

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 06:36:27 ; Search time 1826.14 Seconds  
(without alignments)  
5638.043 Million cell updates/sec

Title: US-09-898-659-1  
Perfect score: 492  
Sequence: 1 atgtatccaacgtagtagata.....atgcagcgatgaccaggtga 492

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vl.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	ID	Description
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1	307	62.4	811	8	AF261775	Lycopers1
2	298.4	60.7	821	8	AF261774	Lycopers1
3	298.4	60.7	127892	8	AF411809	Lycopers1
4	160.2	32.6	61382	8	AF411806	Lycopers1
5	123.6	25.1	683	8	AY072397	Arabidops
6	106.2	21.6	725	8	AY065153	Arabidops
7	105.6	21.5	98942	8	F24J5	Arabidops
8	95	19.3	782	8	AF049928	Arabidops
9	90.8	18.5	103550	2	AP004003	Oryza sat
10	79.2	16.1	78574	8	AP004536	Oryza sat
11	74.2	15.1	146017	2	AP003575	Oryza sat
12	73.6	15.0	132699	8	AC006917	Genomic s
13	71.6	14.6	87459	8	AB015477	Arabidops
14	71.6	14.6	89898	8	AB026658	Arabidops
15	66.8	13.6	469	8	EGU271639	Elaeis gu
16	60.4	12.3	847	8	AF327424	Arabidops
17	58.2	11.8	119091	8	AC016041	Genomic s
18	56.4	11.5	86014	8	F19C14	Sequence
19	56	11.4	46335	8	AC022354	Arabidops
20	46.8	9.5	87885	8	AC007659	Arabidops
21	45.4	9.2	975	8	AY054680	Arabidops
22	45.4	9.2	991	8	ATU78870	Arabidops
23	45	9.1	174264	2	OSN000003	Oryza sat
24	44.4	9.0	70288	8	AC002409	Arabidops
25	41.2	8.4	407	11	G70981	Arabidops
26	40.6	8.3	1865	8	AF367322	Arabidops
27	39.6	8.0	301550	1	AP003134	Staphyloc
28	39.6	8.0	342600	1	AP003363	Staphyloc
29	38.4	7.8	168655	8	AP000969	Oryza sat
30	38	7.7	82261	2	AC066582	Homo sapi
31	38	7.7	112028	2	AC095340	Rattus no
32	38	7.7	131599	8	AC079685	Oryza sat
33	37.6	7.6	111464	8	F10K1	Sequence
34	37	7.5	6612	8	ATU78866	Arabidops
35	37	7.5	48008	8	AB025621	Arabidops
36	36.8	7.5	119420	9	HS997K18	Human DNA
37	36.8	7.5	147114	9	AP001939	Homo sapi
38	36.8	7.5	159670	2	AC027626	Homo sapi
39	36.8	7.5	159660	2	AC098620	Rattus no
40	36.8	7.5	164229	9	AC092671	Homo sapi
41	36.8	7.5	183680	9	AC098859	Homo sapi
42	36.8	7.5	269081	2	AC068493	Mus muscu
43	36.6	7.4	101944	9	AC011463	Homo sapi
44	36.6	7.4	193683	2	AC011590	Homo sapi
45	36.4	7.4	392	11	G71820	Arabidops

ALIGNMENTS

RESULT 1  
AF261775  
LOCUS AF261775 811 bp DNA linear PLN 06-JUN-2000  
DEFINITION Lycopersicon pennellii ORFX (ORFX) gene, complete cds.  
ACCESSION AF261775.1 GI:8272627  
VERSION  
KEYWORDS  
SOURCE Lycopersicon pennellii.  
ORGANISM Lycopersicon pennellii  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
REFERENCE 1 (bases 1 to 811)  
AUTHORS Frary,A., Nesbitt,T.Clint., Frary,A., Grandillo,S., van der  
Knaap,E., Cong,B., Liu,J., Meller,J., Elber,R., Alpert,K.B. and  
Tanksley,S.D.  
TITLE fw2.2: a quantitative trait locus key to the evolution of tomato  
fruit size  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 811)  
AUTHORS Frary,A., Nesbitt,T.Clint., Frary,A., Grandillo,S., van der  
Knaap,E., Cong,B., Liu,J., Meller,J., Elber,R., Alpert,K.B. and

Printed

Tanksley,S.D.  
Direct Submission  
Submitted (28-APR-2000) Plant Breeding, Cornell University, 248  
Emerson Hall, Ithaca, NY 14853, USA

FEATURES  
source  
Location/Qualifiers  
1. .811  
/organism="Lycopersicon pennellii"  
/db\_xref="taxon:28526"  
/note="fw2.2: small-fruit"  
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/gene="ORFX"  
/product="ORFX"  
55..717  
/gene="ORFX"  
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/note="lpORFX"  
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DLEEAPCVDCLVHVFCEPCALCQYRELKNGFDIMGQWQANMDRQSGVTPPYHAG  
MTR"

BASE COUNT 221 a 138 c 169 g 283 t

ORIGIN

Query Match 62.4%; Score 307; DB 8; Length 811;  
Best Local Similarity 80.4%; Pred. No. 7.5e-71;  
Matches 419; Conservative 0; Mismatches 0; Indels 102; Gaps 1;

Qy 1 atgtatccaacgtagataatactaggtcttaataaacaaccttatgtctctctcac 60  
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Db 55 ATGTATCCAACGTAGGATATATCTAGGTCTAATGAACAACCTTATGTCTCTCTCAC 114  
Qy 61 tatgtatctgcccccgccaccacacgcgcggtggtcaactggtcttgcactgtttt 120  
|||||  
Db 115 TATGTATCTGCCCGCCGCCACCACGCGCGTGTCAACTGGTCTTGTCTACTGTTTT 174  
Qy 121 gatgacctctgaactgttttagttactagtgtttgccccttgatacccttggagcagatt 180  
|||||  
Db 175 GATGACCTGCTAACTGTTTTAGTTAGTTAGTTGGCCTTTGTATCATCCTTTGGACAGATT 234  
Qy 181 tctgaataactaacaagaacaactt----- 208  
|||||  
Db 235 TCtGAATACTAAACAAGGAACAACCTTGTAAGTATATATATACACATCTCTTTTTTTT 294  
Qy 209 ----- 208  
Db 295 GGGATAAGTTCAATTTATTTGATATTTGGTTACCAAGAATATGATGTTTGTGCTGTTTC 354  
Qy 209 -----catgtggagtagagtgcaattattttgttctggactgacagagattg 258  
Db 355 TTGATGTTAGCATCTGGGAGTAGAGGTCATATATATTTGTTGCTGGACATGACAGGATTG 414  
Qy 259 cctagcctatatctctctctacaggtctaaaaatgagggggcaaatgatctctgggaagag 318  
|||||  
Db 415 CCTAGCCTATATCTCTGCTTCTACAGGCTCTAAAATGAGGGGCAATATGATCTGGAAGAG 474  
Qy 319 gcaaccttggttgattgctctgtacatgtattctgtgaaccttgctctctttgcccagaag 378  
Db 475 GCACCTTGCTGTGTTGTTCTTGTACATGTTATCTGTGAACCTTGTGCTCTTGTGCCAAGAA 534  
Qy 379 tacagagagccttaagaaccgtgctttgatgggaatagg 419  
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Db 535 TACAGAGAGCTTAAAGAACCGTGGCTTTGATATGGGAATAGG 575

RESULT 2  
AF261774  
LOCUS

DEFINITION  
AF261774  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Lycopersicon esculentum ORFX (ORFX) gene, complete cds.  
AF261774.1 GI:8272625  
tomato.  
Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
1 (bases 1 to 821)  
Frary,A., Nesbitt,T.Clint., Frary,A., Grandillo,S., van der  
Knaap,E., Cong,B., Liu,J., Meller,J., Elber,R., Alpert,K.B. and  
Tanksley,S.D.  
fw2.2: a quantitative trait locus key to the evolution of tomato  
fruit size  
Unpublished  
2 (bases 1 to 821)  
Frary,A., Nesbitt,T.Clint., Frary,A., Grandillo,S., van der  
Knaap,E., Cong,B., Liu,J., Meller,J., Elber,R., Alpert,K.B. and  
Tanksley,S.D.  
Direct Submission  
Submitted (28-APR-2000) Plant Breeding, Cornell University, 248  
Emerson Hall, Ithaca, NY 14853, USA  
Location/Qualifiers  
1. .821  
/organism="Lycopersicon esculentum"  
/db\_xref="taxon:4081"  
/note="fw2.2: large-fruit"  
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/gene="ORFX"  
/product="ORFX"  
56..726  
/gene="ORFX"  
join(56..263,365..574,653..726)  
/gene="ORFX"  
/note="LeORFX"  
/codon\_start=1  
/product="ORFX"  
/protein\_id="AAF74286.1"  
/db\_xref="GI:8272626"  
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NCLVTSVCPCTIFGQISEILNKGTSCSRGALYCLLGLTGLPSLYSCFYRKMGRQY  
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MTR"

BASE COUNT 224 a 138 c 177 g 282 t

ORIGIN

Query Match 60.7%; Score 298.4; DB 8; Length 821;  
Best Local Similarity 79.4%; Pred. No. 1.4e-68;  
Matches 413; Conservative 0; Mismatches 6; Indels 101; Gaps 1;

Qy 1 atgtatccaacgtagataatactaggtcttaataaacaaccttatgtctctctcac 60  
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Db 56 ATGTATCAACGGTAGGATATATCCAGGTCCCAATGAACAACCTTATGTCTCTCTCAC 115  
Qy 61 tatgtatctgcccccgccaccacacgcgcggtggtcaactggtcttgcactgtttt 120  
|||||  
Db 116 TATGTATCTGCCCGCCGCCACCACGCGCGTGTGCGACTGGTCTTGTCTATTGTTTT 175  
Qy 121 gatgacctctgaactgttttagttactagtgtttgccccttgatacccttggagcagatt 180  
|||||  
Db 176 GATGACCTGCTAACTGTTTAGTTAGTTAGTTGGCCTTTGTATCATCCTTTGGACAGATT 235  
Qy 181 tctgaataactaacaagaacaactt----- 208  
|||||  
Db 236 TCtGAATACTAAACAAGGAACAACCTTGTAAGTATATATACACTTTTTTTTGGGGGGGG 295  
Qy 209 ----- 208  
Db 296 GGATAAATCAATTTATTTGATATTTGGTTACCAAGAAATATGATGTTGTGTTGTTTCT 355

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QY 209 -----catgtggagtagagtgcatattattgttctgggactgcacagattgc 259
Db 356 TGATGTTAGCATGTGGGAGTAGAGTGCAATTATATTGTTGCTGGGATTTGACAGATTGC 415
QY 260 ctagcctattccctgcttctcacaggtctaaatagaggggccaatatgatctgggaaggg 319
Db 416 CTAGCCTATATTCCTGCTCTACAGGTCTAAATAGAGGGGCAATATGATCTGGAAGAGG 475
QY 320 caccctgtgtgatgtctctgtacatgtattctgtgaacctgtgctctttgccagaat 379
Db 476 CACCTGTGTGATGTCTTGTACATGATATCTGTGAACCTTGCTCTTTGCCAAGAAAT 535
QY 380 acagagagcttaagaacctggcctttgatgggaatagg 419
Db 536 ACAGAGAGCTTAAGAACCGTGGCTTTGATATGGGAATAGG 575

RESULT 3
AF411809/c 127892 bp DNA linear PLN 07-OCT-2001
LOCUS Lycopersicon esculentum BAC clone FW2.2, complete sequence.
DEFINITION AF411809
ACCESSION AF411809
VERSION AF411809.1 GI:15987774
KEYWORDS tomato.
SOURCE Lycopersicon esculentum
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 127892)
AUTHORS van der Hoeven,R.S. and Tanksley,S.D.
TITLE Deductions about the number, organization and evolution of genes in
the tomato genome based on analysis of large EST collection and
selective genomic sequencing
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 127892)
AUTHORS Nesbitt,C.T., van der Hoeven,R.S. and Tanksley,S.D.
TITLE Direct Submission
JOURNAL Submitted (20-AUG-2001) Plant Breeding, Cornell University, 252
Emerson Hall, Ithaca, NY 14850, USA
FEATURES
source
Location/Qualifiers
1..127892
/organism="Lycopersicon esculentum"
/db_xref="taxon:4081"
/clone="FW2.2 BAC"
BASE COUNT 42761 a 20070 c 20496 g 44565 t
ORIGIN

Query Match 60.7%; Score 298.4; DB 8; Length 127892;
Best Local Similarity 79.4%; Pred. No. 7.2e-69;
Matches 413; Conservative 0; Mismatches 6; Indels 101; Gaps 1;

QY 1 atgtatccaacggtaggatataatctaggtctaatgaacaaccttatgttctctctcac 60
Db 19179 ATGTATCAAAACGGTAGGATATAATCAGGTCCAATGAACAACCTTATGTTCTCTCTCAC 19120
QY 61 tatgtatctgccccggcaccacacacgcgcggtgtgtaacctgtctttgtcaactgtttt 120
Db 19119 TATGTATCTGCCCCGGCACACCACCGCGGTGGTGCAGCTGGTCTTTGTGCATTTGTTT 19060
QY 121 gatgacctgctaaactgttttagttactagtgtttgcccttgtatcacctttggacagatt 180
Db 19059 GATGACCTTGCTAACTGTTTACTTACTAGTGTTCCTTGTATCACCTTTGGACAGATT 19000
QY 181 tctgaataactaatacaaaagggaacaactt----- 208
Db 18999 TCTGAATAACTAAACAAGGAACAACCTTCTAAGTATATACACTTTTTTTTTTGGGGGGGG 18940
QY 209 ----- 208
Db 18939 GGATAAATCAATTTATTGATATTGGTTACCAAGAATAATGATGTTTGTGTTTCT 18880
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QY 260 ctagcctattccctgcttctcacaggtctaaatagaggggccaatatgatctgggaaggg 319
Db 18819 CTAGCCTATATTCCTGCTCTACAGGTCTAAATAGAGGGGCAATATGATCTGGAAGAGG 18760
QY 320 caccctgtgtgatgtctctgtacatgtattctgtgaacctgtgctctttgccagaat 379
Db 18759 CACCTGTGTGATGTCTTGTACATGATATCTGTGAACCTTGCTCTTTGCCAAGAAAT 18700
QY 380 acagagagcttaagaacctggcctttgatgggaatagg 419
Db 18699 ACAGAGAGCTTAAGAACCGTGGCTTTGATATGGGAATAGG 18660

RESULT 4
AF411806 61382 bp DNA linear PLN 07-OCT-2001
LOCUS Lycopersicon esculentum BAC clone Clemson_Id 207, partial sequence.
DEFINITION AF411806
ACCESSION AF411806
VERSION AF411806.1 GI:15987771
KEYWORDS tomato.
SOURCE Lycopersicon esculentum
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 61382)
AUTHORS van der Hoeven,R.S. and Tanksley,S.D.
TITLE Deductions about the number, organization and evolution of genes in
the tomato genome based on analysis of large EST collection and
selective genomic sequencing
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 61382)
AUTHORS van der Hoeven,R.S. and Tanksley,S.D.
TITLE Direct Submission
JOURNAL Submitted (20-AUG-2001) Plant Breeding, Cornell University, 252
Emerson Hall, Ithaca, NY 14850, USA
FEATURES
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Location/Qualifiers
1..61382
/organism="Lycopersicon esculentum"
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ORIGIN

Query Match 32.6%; Score 160.2; DB 8; Length 61382;
Best Local Similarity 90.6%; Pred. NO. 3.2e-32;
Matches 193; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

QY 209 catgtggagtagagtgcatattattgttctgggactg-acagagattgcctagccta 267
Db 21362 CATGTGCTAGTAGAGCTGCATTTATGTTGTTGGGACTGAACAGGATTGCTTACCTTA 21421
QY 268 tttctcgtctctcacaggtctaaatagaggggccaatatgatctggaagagcaccttgt 327
Db 21422 TATTCCTACTTCTATAGGTCCAAATAGAGGGCAATGTGATCTGGAAGAGCACCTTGT 21481
QY 328 gttgattgtcttgtaca-tgtattctgtgaacctgtgctctttgccagaatacacaga 386
Db 21482 GCGGATTGCTTTGAACATTTGATTCTGTGAACCTTTGTGCTCTTATCCAAGAGACAGAGA 21541
QY 387 gcttaagaacctggcctttgatagggaatagg 419
Db 21542 GCTTAAGAACCTTGCTTTAATATGGGAATAGG 21574
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RESULT 5
AY072397
LOCUS Arabidopsis thaliana unknown protein (Atlg14870) mRNA, complete
DEFINITION
cds.
ACCESSION AY072397.1 GI:18252924
VERSION AY072397.1
KEYWORDS FLI_CDNA.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 683)
Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B., Miranda,M.,
Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
Direct Submission
Submitted (02-JAN-2002) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
e-mail for correspondence: arab@sequence.stanford.edu

COMMENT
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGECC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Nguyen,M.,
Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J.,
Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K.,
Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,
Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

Nguyen,M. (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed
equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.
(SSP/Stanford) contributed equally to this work as PIs.

FEATURES
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ecotype: Columbia"
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BASE COUNT 176 a 129 c 148 g 230 t
ORIGIN

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Best Local Similarity 61.3%; Pred. No. 3e-22;
Matches 217; Conservative 0; Mismatches 134; Indels 3; Gaps 1;

Qy 34 tggtaactggtcttctgactgtttgtgatgacctgtaactgttagtactagtgtt 153
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Db 110 TGGTCCACAGGCTCTCTGATTCGTTCTGACTGCACAAAATTGTTGTATCACATCTG 169

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/translacion="MEKOWTSGLFSCHEMDESETACLTFCPCPVTFGRADISDEGRGCG
GRCCVFGLCVGVGLPCFLFSCYTRKIRSKFGLPESPTSDCVTHFFCECCALCQEH
ELKTRGLDPSIGSGNMORTMAPPMQOMMG"
BASE COUNT      217 a 131 c 152 g 225 t
ORIGIN

Query Match      21.6%; Score 106.2; DB 8; Length 725;
Best Local Similarity 58.4%; Pred. No. 1.2e-17;
Matches 205; Conservative 0; Mismatches 143; Indels 3; Gaps 1;

Qy 90 gcggtggtcaactggctttgtcaactgttttgatgacacctgctaaactgttagttactag 149
Dy 133 GCAATGGACTTCTGGCTCTTTTCAGCTGCATGGAAGACAGTGAACACTGCTGCCTCACATG 192
Qy 150 tgtttgacctgtatcaccttggacagatcttgaataactaaacaagaacaacttc 209
Dy 193 TTTGTGCCCATCGCTCACTTTTCGACGAGTCCGGACATTTCCGACGAAGAAGACCGG 252
Qy 210 atgtgggagtgagtgcatattgtttgct---gggactgacaggattgcctagcct 266
Dy 253 TTGTGGGAGATGTGGGTATTTTACGGGCTAATATGTTGTGTGGTGGCTTACCTTGCTT 312
Qy 267 atattcgtcttctacaggtctaaatgaggggccaataatgatctggaggggcaacttg 326
Dy 313 GTTCTCATGCTTACCGGACCAAGATCCGAAGCAAAATTCGGGTACCGGAGTCTCCAAAC 372
Qy 327 tgttgattgcttggacatgattctgtgaacctgtgctcttcttggcgaagatacagaga 386
Dy 373 TTCGGATGCGTCACTCACTCTTTTGTGATGTGTGCTCTTGGCCGAAGAACCCGTGA 432
Qy 387 gcttaagaacctggcttggatggtggaatggggtggcgaactaatatgga 437
Dy 433 ACTCAAAACCGGTCTCTTGACCCCTCTATTGGGTGGAGTGGAATATGCA 483

RESULT 7
F24J5/c
LOCUS      F24J5
DEFINITION Arabidopsis thaliana chromosome 1 BAC F24J5 sequence, complete
sequence.
ACCESSION AC008075
VERSION   AC008075.2 GI:5724802
KEYWORDS  HTG.
SOURCE    thale cress.
ORGANISM  Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 98942)
Vysotskaya,V.S., Schwartz,J.R., Yu,G., Toriumi,M., Lenz,C., Liu,S.,
Lee,J.M., Li,J., Gonzalez,A., Liu,A., Liu,K., Vaysberg,M.,
Sakano,H., Chin,C., Choi,E., Chlou,J., Altafi,H., Araujo,R.,
Brooks,S., Buehler,E., Chao,Q., Conn,L., Conway,A.B., Dunn,P.,
Hansen,N., Howng,B., Huizar,L., Khan,S., Kim,C., Palm,C.,
Rowley,D., Shinn,P., Walker,M., Davis,R.W., Ecker,J.R.,
Federstepel,N.A. and Theologis,A.
The sequence of BAC F24J5 from Arabidopsis thaliana chromosome 1
Unpublished
2 (bases 1 to 98942)
Theologis,A.
Direct Submission
Submitted (19-JUL-1999) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
3 (bases 1 to 98942)
Theologis,A.
Direct Submission

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

Submitted (10-AUG-1999) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
4 (bases 1 to 98942)
Theologis,A.
Direct Submission
Submitted (17-AUG-1999) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
On Aug 10, 1999 this sequence version replaced gi:5525042.
The sequence of BAC F24J5 from Arabidopsis thaliana chromosome 1.
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2103..2171,2251..2329,2407..2483,2575..2713,2899..3039,
3364..3386,3492..3728,3827..3952,4035..4136,4212..4358,
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MLDFFMADQLCSQVPMRLNLEYITACYTIGSATQDYECMRVKRYLAYAVSFLPY
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/gene="F24J5.5"  
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SSGEFESDTEDEEDVEITYRENVRSEKKVVDOSAKRLKSKAEASOMHKKRRKRDSEST  
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VGHWCYRIRISTMICYFFYKNITFGFTLFLYETVYTFSTPAYNDWFLSYNVFESSL  
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Query Match 21.5%; Score 105.6; DB 8; Length 98942;  
Best Local Similarity 58.5%; Pred. No. 8.8e-18;  
Matches 227; Conservative 0; Mismatches 149; Indels 12; Gaps 2;

QY 94 tgggtcaactggtctgttgcactgtttttgatgaccctgcttaactgttttagttactagtgt 153  
Db 65547 TGGTCGACTGATTGTTGTGAATGTTGGATGCACATAAATCATGCTGCTTGCATTGTTGG 65488

QY 154 tggccttgatcaccttttgacagattctgaaataactaaacaaagaaacacttcagt 213  
Db 65487 TGCCCCTTGTTGCCCTTGGACGATCGCGGAGGTGTGTAGACAGAGGTTCACATCGTGT 65428

QY 214 gggagtagaggtgcattatat-----tgttgctgggactgacagattgcctagc 264  
Db 65427 GGTGTGACGCGGGGATGTACATGATCATATTGTTGACCGGGTATGAGGAAGCAGT 65368

QY 265 ctatatctctctctacaggtcttaaatgaggggccaatatgatctggaagaggcacct 324  
Db 65367 CTCTACTCTTGTCTTACCGAACCAACTTAGAGCCCAATACATCAATCTCAAGGAGAGACCT 65308

QY 325 tgtgttgattgtctgtacatgtattctgtgaacctgtgtcttgcgaagatacaga 384  
Db 65307 TGTGTGACTGTTGTGTCCACTTTTGTGTGCGAGCCATGCGCTCTTTGTCAGAGATATAGG 65248

QY 385 gagctt---aagaaccgtggctttgatggaatagggtggcaagctaataatggataga 441  
Db 65247 CAACTTCAACACAAACCGGATTTGGACTTGGTCATCGGTGGCATGGATATGGAACGA 65188

QY 442 caaagccggggagttaaccatgcacctt 469  
Db 65187 CATGCACGACTTGTGCTCTACACCTT 65160

RESULT 8  
AF049928  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AF049928 782 bp mRNA linear PLN 05-JUL-2000  
Petunia x hybrida PGPS/d12 (PGPS/d12) mRNA, complete cds.  
AF049928  
AF049928.1 GI:4105793  
Petunia x hybrida.  
Petunia x hybrida  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Petunia.  
1 (bases 1 to 782)  
Guyon,V.N., Astwood,J.D., Garner,E.C., Dunker,A.K. and Taylor,L.P.

**TITLE**  
Isolation and characterization of cDNAs expressed in the early stages of flavonol-induced pollen germination in petunia

**JOURNAL**  
Plant Physiol. 123 (2), 699-710 (2000)

**MEDLINE**  
20317212

**PUBMED**  
10859200

**REFERENCE**  
2 (bases 1 to 782)

**AUTHORS**  
Guyon, V., Astwood, J.D. and Taylor, L.P.

**TITLE**  
Direct Submission

**JOURNAL**  
Submitted (23-FEB-1998) Genetics and Cell Biology, Washington State University, Science Hall, Pullman, WA 99164-4234, USA

**FEATURES**  
Location/Qualifiers

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BASE COUNT
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RESULT	9
accession	2004003/c
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DEFINITION	AP004003 103550 bp DNA linear HTG 02-AUG-2001
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	PROGRESS ***, in ordered pieces.
	AP004003
ACCESSION	AP004003.1 GI:15076811
VERSION	HTG; HTGS_PHASE2.
WORDS	Oryza sativa (cultivar:Nipponbare) DNA, clone:OJ1124_H01..
SOURCE	Oryza sativa
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Orzyeae; Oryza.

REFERENCE	1 (bases 1 to 103550)
AUTHORS	Sasaki,T., Matsumoto,T. and Yamamoto,K.
TITLE	Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC clone:OJ1124_H01
JOURNAL	Published Only in Database (2001) In press
REFERENCE	2 (bases 1 to 103550)
AUTHORS	Sasaki,T., Matsumoto,T. and Yamamoto,K.
TITLE	Direct Submission
JOURNAL	Submitted (01-AUG-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
COMMENT	(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468) The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data. NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved. * NOTE: This is a 'working draft' sequence. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved. Location/Qualifiers 1. 103550 /organism="Oryza sativa" /cultivar="Nipponbare" /db_xref="taxon:4530" /chromosome="2" /clone="OJ1124_H01" 29755 a 21927 c 21786 g 30082 t
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BASE COUNT	
ORIGIN	

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QY 197	aaggaaacaacttcattggtggagtagagtgacattatattttgctgggactg--acag	253		
Db 5606	GGGGGTGCTGCTGTCGGGGACAGACGGGTGCTGTACGGCGTGGTTCCTGTCACGG	5547		
QY 254	gattgcctagcctatatctcgtctcacaggtctcaaaatgagggggaataatgatctgg	313		
Db 5546	GCTGCAGCTGTATCTACTCTCTGATCTACCGCTCCACAGCTGCGGTCCGACGTACGGCGTCG	5487		
QY 314	aagaggcaccttggttgattgattgtttgtacatgattctctgtaaacctttgtgctctttgcc	373		
Db 5486	AGGAGAGCGCCCTGCCCGACTGCCTGCTCCACTTGTGGTGGGAGCCCTGCGCCCTCTGCC	5427		
QY 374	agaatacacagagagcttaagaacccgtgctttgatatagggaatagg	419		
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RESULT	10
AP004536	
LOCUS	
DEFINITION	78574 bp DNA linear PLN 14-DEC-2001 Lotus japonicus genomic DNA, chromosome 4, clone:Ljt15N19, TM0097b, complete sequence.
ACCESSION	AP004536
VERSION	AP004536.1 GI:17736903
KEYWORDS	HTG.
SOURCE	Lotus japonicus DNA, clone_lib:LjT library clone:Ljt15N19. Lotus japonicus
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurousids I; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.

REFERENCE 1 (sites)  
AUTHORS Sato,S., Kaneko,T., Nakamura,Y., Asamizu,E., Kato,T. and Tabata,S.  
TITLE Structural Analysis of a Lotus japonicus Genome. I. Sequence Features and Mapping of Fifty-six TAC clones which cover the 5.4 Mb Regions of the Genome

JOURNAL unpublished  
REFERENCE 2 (bases 1 to 78574)  
AUTHORS Nakamura,Y.  
TITLE Direct Submission  
JOURNAL Submitted (13-DEC-2001) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 252-0812, Japan (E-mail:ynakam@kazusa.or.jp, URL:http://www.kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)

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ORIGIN

Query Match 16.1%; Score 79.2; DB 8; Length 78574;  
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Matches 135; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 192 aaacaaggaacactcatctgaggatagaggtgcattatattgttctgggaactgac 251  
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QY 252 aggattgcctagcctattctctgcttcctacaggtctaaatgagggggcaatatgatct 311  
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Db 11485 TGGTTCGGGTGCTGTGTACTCATCTCTCCGCTTCCAAGTTGAGAGCCCAATACATGTT 11544

QY 312 ggaagagacccttgcttgaatgctcttgatcatgtattcttggaacctgtgctctttg 371  
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QY 372 ccaagaatacagagagcttaagaaccctggctttgatatgggaatagg 419  
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Db 11605 CCAAGAGTATCGTGAGCTTGAAATCGTGGATTGTGACATGACCTTAGG 11652

RESULT 11  
LOCUS AP003575/c  
DEFINITION Oryza sativa chromosome 6 clone P0528B02, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in ordered pieces.  
ACCESSION AP003575  
VERSION AP003575.1 GI:113936415  
KEYWORDS HTG; HTGS\_PHASE2.  
SOURCE Oryza sativa (cultivar:Nipponbare) DNA, clone:P0528B02.  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (sites)  
AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.  
TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC clone:P0528B02  
JOURNAL Published Only in DataBase (2001) In press  
REFERENCE 2 (bases 1 to 146017)  
AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.  
TITLE Direct Submission  
JOURNAL Submitted (02-MAY-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan



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REFERENCE
AUTHORS      3 (bases 1 to 132699)
TITLE        Ecker,J.R.
JOURNAL      Submitted (07-MAY-1999) Arabidopsis thaliana Genome Center,
              Department of Biology, University of Pennsylvania, 38th Street and
              Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
REFERENCE
AUTHORS      4 (bases 1 to 132699)
              Cheuk,R., Shinn,P., Brooks,S., Buehler,E., Chao,Q.,
              Johnson-Hopson,C., Khan,S., Kim,C., Altafi,H., Bei,B., Chin,C.,
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              Yu,G., Davis,R., Federspiel,N., Theologis,A. and Ecker,J.
TITLE        Direct Submission
JOURNAL      Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center,
              Department of Biology, University of Pennsylvania, 38th and
              Hamilton Walk, Philadelphia, PA 19104-6018, USA
COMMENT      On May 7, 1999 this sequence version replaced gi:4731042.
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RESULT 13
AB015477
LOCUS AB015477 87459 bp DNA linear PLN 27-DEC-2000
DEFINITION Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MOK9.
ACCESSION AB015477 BA000015
VERSION AB015477.1 GI:3241925
KEYWORDS Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui P1
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ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (sites)
Nakamura,Y., Sato,S., Asamizu,E., Kaneko,T., Kotani,H., Miyajima,N.
and Tabata,S.
Structural analysis of Arabidopsis thaliana chromosome 5. VII.
Sequence features of the regions of 1,013,767 bp covered by sixteen
physically assigned P1 and TAC clones
DNA Res. 5 (5), 297-308 (1998)
99087489
2 (bases 1 to 87459)
Nakamura,Y.
Direct Submission
Submitted (17-JUN-1998) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)

Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=WOK9
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://combio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlin1.cool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is K21B8 and the 3' clone is K2K18.

FEATURES
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Qy 266 tataattcctgtcttcacaggtcctaaaaatgaggggcaataatgatcttgaaagagcaccctt 325  
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Qy 326 gtgtgtattgtctgtcacatgattctgtgaaccttgcctcttgcacagaatacacagag 385  
Db 46362 GTACTGATTGCTTAAACATTTCTGCTGTGAGCTTTGCTTTTGACACAGAATACCGTG 46421  
Qy 386 agctaaagaacgtggtcttgatatgggaataag 419  
Db 46422 AACTCAGCACCAGCGGTTTCATATGATGATGCTTGG 46455  
RESULT 14  
AB026658/c  
LOCUS 88989 bp DNA linear PLN 27-DEC-2000  
DEFINITION Arabidopsis thaliana genomic DNA, chromosome 3, pl clone: MYF24.  
ACCESSION AB026658 BA000014  
VERSION AB026658.1 GI:4757414  
KEYWORDS  
SOURCE Arabidopsis thaliana (strain:Columbia) DNA, clone\_lib:Mitsui pl  
clone:MYF24.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi  
1 (sites)  
Sato,S., Nakamura,Y., Kaneko,T., Katoh,T., Asamizu,E. and Tabata,S.  
Structural analysis of Arabidopsis thaliana chromosome 3. I.  
Sequence features of the regions of 4,504,864 bp covered by sixty  
pl and TAC clones  
DNA Res. 7 (2), 131-135 (2000)  
JOURNAL 20277480  
MEDLINE  
REFERENCE 2 (bases 1 to 88989)  
AUTHORS Sato,S., Nakamura,Y., Kaneko,T., Kato,T., Asamizu,E. and Tabata,S.  
TITLE Direct Submission

## JOURNAL

Submitted (28-APR-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)

## COMMENT

Address for correspondence: kaos@kazusa.or.jp  
For the latest information on annotation of this clone, please see [http://www.kazusa.or.jp/kaos/cgi-bin/agd\\_graph.cgi?c=MYF24](http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MYF24)  
Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.  
The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, <http://compbio.ornl.gov/Grail-1.3/>), GENSCAN (Chris Burge, MIT, <http://CCR-081.mit.edu/GENSCAN.html>), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, <http://www.cbs.dtu.dk/services/NetGene2/>) and SplicePredictor (Volker Brendel, Stanford University, <http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi>).  
Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, <http://genome.wustl.edu/eddy/tRNAscan-SE/>).  
This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is M1E15 and the 3' clone is K24M9.

## FEATURES

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1. .88989  
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/strain="Columbia"  
/db\_xref="taxon:3702"  
/chromosome="3"  
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/clone="MYF24"  
1511. .2335

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KMRTESSDKSEFSLICEHLCKKICGFKGRSASITAVFENTNSPTSVFDIA  
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SKWSKQOQVGVVPLVPLITLHEFHNCLNSQEOFSPEAEFYNRCNOISKATR  
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gene\_id:MYF24.4  
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## CDS

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BKGVLPFPQCVHGFASRLSAGDEKLLSLLVGDSTSTNTLMTVTSIGEANVSW  
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## CDS

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## CDS

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NSSNNVWNLMTLSPIDPFSFHLQSLDYSIFHDMTLILCCDDNQTGVCGCIIFARGD  
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Join(15639. .15823,16070. .16304,16383. .16552,16639. .16778,  
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LILSVYWDPTKSSVFCLLTFLIWRGLVYVAFALSAFLFAFWLRCFRSEKLM  
ELKVTAPMNTMEOLLAVONGI SELEONIQDANIVLLKFRALLSLPQASQKFAIA  
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## CDS

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/evidence=not\_experimental

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CDS  
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ILRSPSKSEIGRSGSSNSRPVQTFVEVELQLSRTEMKSGPNAPVOSTFNML  
HDNFTLFLNLYENRPGSVRYDSLASCEVMKYVGGDDSTPMFVAVGSDNGVIKHAFC  
GOETEMVPEGVSSGELTVRLLEKWHFSDGSHLSVNSSSLSLSDSSALSKTG  
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Db 51568 CTTGTGCGACAGGTGGGTGTGTATGGAATGATATTTTTCATCGAGTGGCGTTGCT 51509  
Qy 269 attctcgtcttacaggtctctaaatgaggggcaaatatgatctctggaagagggcacccttg 328  
Db 51508 ACTCATGTGATGTTCCGGGCCAAAATGCGAAACAAATACGGGTACCGGATGTCGCGCTC 51449  
Qy 329 ttgattgtctgtacatgtattctgtgaacctgtgtctcttgcacaaataacagagagc 388  
Db 51418 CCGATTGGATCAGTCACATTATCTGTGAGCAATGCGCTCTTTGTCAAGAGTATCGTGAGC 51389  
Qy 389 ttaagaacccgtggcttgatgggaatagggtggcaagcgaatgatggat 438  
Db 51388 TCAACACCGTGGTTTTCACCCCAATATGTTGAATTTTATTATTAATGAAT 51339

RESULT 15  
EGU271639/c  
LOCUS EGU271639 469 bp DNA linear PLN 06-JAN-2001  
DEFINITION Elaeis guineensis microsatellite DNA, clone mEgCIR0230.  
ACCESSION AJ271639  
VERSION AJ271639.1 GI:12053789  
KEYWORDS microsatellite; repetitive DNA.  
SOURCE Elaeis guineensis.  
ORGANISM Elaeis guineensis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Areaceae; Arecoidae;  
Coccolae; Elaeidinae; Elaeis.  
1 (bases 1 to 469)  
Billette,N., Risterucci,A.M., Barcelos,E., Amblard,P. and  
Baurens,F.C.  
Development, characterization and across-taxa transferability of  
Elaeis guineensis SSR markers  
Unpublished

REFERENCE 2 (bases 1 to 469)  
AUTHORS Billette,N.  
TITLE Direct Submission  
JOURNAL Submitted (02-FEB-2000) Billette N., CP. Cirad, BP Avenue Agropolis  
F-34032 Montpellier CEDEX 1, 34032, FRANCE  
FEATURES  
Location/Qualifiers  
source  
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/cultivar="LA ME"  
/isolate="Tenara palm"  
/db\_xref="taxon:51953"  
/clone="mEgCIR0230"  
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/note="Reverse primer"  
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Best Local Similarity 60.3%; Pred. No. 3.5e-07;  
Matches 129; Conservative 0; Mismatches 82; Indels 3; Gaps 1;  
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Db 449 CATGTGGACAGCTGGAGCGCTATATGTGATTCTTAAGGTCTTGACTAGGTGTCACATGGA 390  
Qy 266 tatattcctgtcttacaggtctctaaatgaggggcaaatatgatctctggaagagggcaccctt 325  
Db 389 TATACTCGTGGTCTTACAGATCCAAAGCTCAGATTGCAACTTGCCTGCGGATTCCTCCCTT 330  
Qy 326 gtgttgattgtctgtacatgtattctgtgaacctgtgtctcttgcacaaataacagag 385  
Db 329 GCTGCGACTGCTGTGTTTACATTTTCTCGGAGTGTGCTGCGCTTGTGTCAAGAGTATACAG 270  
Qy 386 agcttaagaacccgtggcttgatgggaatagg 419  
Db 269 AGCTCAGAACCGTGGATGATGATGACTATAGG 236  
Search completed: July 15, 2002, 08:28:45  
Job time: 6738 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 06:36:27 ; Search time 1598.68 Seconds  
(without alignments)  
4153.741 Million cell updates/sec

Title: US-09-898-659-1  
Perfect score: 492  
Sequence: 1 atgtatccaacggtaggata.....atgcaggatgaccagggtga 492

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues  
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST.\*  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estnu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_htc.\*  
9: gb\_estl.\*  
10: gb\_estc.\*  
11: gb\_htc.\*  
12: gb\_gss.\*  
13: em\_gss\_hum.\*  
14: em\_gss\_inv.\*  
15: em\_gss\_pln.\*  
16: em\_gss\_vrt.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	165.6	33.7	610	10	BG459056
2	153	31.1	559	9	AI897534
3	153	31.1	585	9	AI778836
4	153	31.1	585	9	AW455311
5	153	31.1	633	9	AI778763
6	153	31.1	673	10	BI922710
7	153	31.1	719	9	AI778764
8	153	31.1	720	9	AI778837
9	151.4	30.8	544	9	AW040794
10	151.4	30.8	620	9	AI775220
11	151.4	30.8	624	9	AW092086
12	150.4	30.6	585	9	AW039653
13	149	30.3	711	10	BI922592
14	148.4	30.2	525	9	AI773903
15	147.6	30.0	415	10	BM176887
16	146.8	29.8	489	9	AW288052
17	146.8	29.8	568	10	BF519667

#### ALIGNMENTS

#### RESULT 1

BG459056

LOCUS

DEFINITION

ACCSSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BASE COUNT

ORIGIN

18 146.8 29.3 638 10 BI264661  
19 146.8 29.3 645 10 BF646652  
20 146.8 29.3 659 10 BG455061  
21 146.8 29.3 683 10 BI263865  
22 146.8 29.3 701 10 BG584553  
23 146 29.7 499 10 BM177616  
24 146 29.7 531 10 BM178944  
25 146 29.7 555 10 BM143404  
26 146 29.7 556 10 BM143488  
27 146 29.7 556 10 BM177498  
28 145 29.5 698 9 AW906026  
29 144.4 29.3 491 10 BM187610  
30 144.4 29.3 551 10 BM188361  
31 144.4 29.3 565 10 BM188873  
32 144.4 29.3 573 10 BM188528  
33 143.8 29.2 566 10 BI123932  
34 142.4 28.9 649 10 BG448256  
35 141.2 28.7 543 9 AW781893  
36 140.6 28.6 548 10 BI432374  
37 140.2 28.5 555 9 AW756955  
38 139.6 28.4 564 10 BE805908  
39 139 28.3 506 10 BI434528  
40 139 28.3 533 9 AI484746  
41 138.4 28.1 698 10 BI433103  
42 132.8 27.0 577 9 AJ407430  
43 132.2 26.9 648 10 BF647753  
44 131.6 26.7 515 10 BG510727  
45 131.4 26.7 529 9 AI960277

BG459056 610 bp mRNA linear EST 19-MAR-2001  
00829 leafy spurge Lambda HybrizAP 2.1 two-hybrid vector cDNA  
Library Euphorbia esula cDNA clone 35AE 5' similar to ORFX  
[Lycopersicon esculentum], accession# AAF74286, mRNA sequence.

BG459056  
BG459056.1 GI:13382381

EST.

leafy spurge.

Euphorbia esula

Eukaryote: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Malpighiales; Euphorbiaceae; Euphorbia.

1 (bases 1 to 610)

Anderson, J.V. and Horvath, D.P.

Identification of mRNAs expressed in underground adventitious buds

of Euphorbia esula (leafy spurge)

Unpublished (2000)

Contact: Anderson JV

Plants Science Research

USDA/ARS, Biosciences Research Lab

1605 Albrecht Blvd., PO Box 5674, Fargo, ND 58105, USA

Tel: 701 239 1263

Fax: 701 239 1252

Email: andersjv@fargo.ars.usda.gov

Seq primer: pAD5.

Location/Qualifiers

1..610

/organism="Euphorbia esula"

/db\_xref="taxon:3993"

/clone\_lib="leafy spurge Lambda HybrizAP 2.1 two-hybrid

vector cDNA Library"

/tissue\_type="underground adventitious buds"

/dev\_stage="3-day induced (decapitated)"

166 a 148 c 146 g 148 t 2 others





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/tissue_type="leaf"
/dev_stage="4-week old"
/lab_host="SOLR"
/notes="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
XhoI; cLES - Tomato Pseudomonas Susceptible EST Library.
Directionally cloned cDNAs inserted into pBlueScript SK(-)
) at 5' end with EcoRI and 3' end with XhoI site"
BASE COUNT 171 a 91 c 119 g 204 t
ORIGIN

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Query Match 31.1%; Score 153; DB 9; Length 585;
Best Local Similarity 64.7%; Pred. No. 2e-35;
Matches 244; Conservative 0; Mismatches 130; Indels 3; Gaps 1;

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DB 148 TGGTCTACTGGGCTTTGTGATGTTCTCTGATATCTCGAGTTGTTGTTAACTTGCTGG 207
QY 154 tgccttgatcaccttggacagattctgaaatactaaacaaagaaacaaacttcatgt 213
DB 208 TGTCCATGATATACATTTGGCAAAATTCGTAATTCGCAAAAGGAACAGTTCTTGT 267
QY 214 ggaagtagaggtgcattatattgttgc---gggactgcagagattgcctagcctatat 270
DB 268 GGTGCAAGTGGAGCTTTATATTTTAAATAGAAGCATTAACAGGATGTGGATGATTTAT 327
QY 271 tctgctctcacaggtctaaataggggcaatatgactggaagagggcaccttgtgtt 330
DB 328 TCATGTTTTTATCGTACAAAATAGAAAAACAATACATGTTACCAAGAACCCCTTGTGGG 387
QY 331 gattgtcttgacatgtattctgtgaacctgtgctcttggccaaagaatacacagagcctt 390
DB 388 GACTGTTTGTCTCATTTTGTGTGATGTTGCTTTATGCCAAGAACATCGTGAACCT 447
QY 391 aagaacgctggcttggataggaaggtggcaagcctaataatggatagacaaagccgg 450
DB 448 AACATCGTGGATGATGATGCTCTATTGTTGGCAAGGAATATGGATAACCAAAATGGA 507
QY 451 ggaattaccatgcccc 467
DB 508 GGAATAGCAATGGCTCC 524

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RESULT 4
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LOCUS EST311849 tomato root during/after fruit set, Cornell University
DEFINITION Lycopersicon esculentum cDNA clone cLEX10111 5', mRNA sequence.
ACCESSION AW455311
VERSION AW455311.1 GI:7008998
KEYWORDS EST.
SOURCE Lycopersicon esculentum
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 585)
AUTHORS van der Hoeven,R.S., Garvin,D., Matern,A.L., Holt,I.E., Liang,F.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.,
Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
TITLE Generation of ESTs from tomato root tissue
JOURNAL Unpublished (1999)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES Location/Qualifiers
source 1..585
/organism="Lycopersicon esculentum"

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/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEX10111"
/clone_lib="tomato root during/after fruit set, Cornell
University"
/tissue_type="root"
/dev_stage="plants during and after fruit-set"
/notes="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Tanksley; Tissue supplied by Dave Garvin
(USDA-ARS, Ithaca, NY 14850)."
BASE COUNT 171 a 91 c 119 g 204 t
ORIGIN

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Query Match 31.1%; Score 153; DB 9; Length 585;
Best Local Similarity 64.7%; Pred. No. 2e-35;
Matches 244; Conservative 0; Mismatches 130; Indels 3; Gaps 1;

QY 94 tggctcaactggtcttctgacactgttttgatgacccctgtaactgttttagttactagtgtt 153
DB 148 TGGTCTACTGGGCTTTGTGATGTTCTCTGATATCTCGAGTTGTTGTTAACTTGCTGG 207
QY 154 tgccttgatcaccttggacagattctgaaatactaaacaaagaaacaaacttcatgt 213
DB 208 TGTCCATGATATACATTTGGCAAAATTCGTAATTCGCAAAAGGAACAGTTCTTGT 267
QY 214 ggaagtagaggtgcattatattgttgc---gggactgcagagattgcctagcctatat 270
DB 268 GGTGCAAGTGGAGCTTTATATTTTAAATAGAAGCATTAACAGGATGTGGATGATTTAT 327
QY 271 tctgctctcacaggtctaaataggggcaatatgactggaagagggcaccttgtgtt 330
DB 328 TCATGTTTTTATCGTACAAAATAGAAAAACAATACATGTTACCAAGAACCCCTTGTGGG 387
QY 331 gattgtcttgacatgtattctgtgaacctgtgctcttggccaaagaatacacagagcctt 390
DB 388 GACTGTTTGTCTCATTTTGTGTGATGTTGCTTTATGCCAAGAACATCGTGAACCT 447
QY 391 aagaacgctggcttggataggaaggtggcaagcctaataatggatagacaaagccgg 450
DB 448 AACATCGTGGATGATGATGCTCTATTGTTGGCAAGGAATATGGATAACCAAAATGGA 507
QY 451 ggaattaccatgcccc 467
DB 508 GGAATAGCAATGGCTCC 524

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RESULT 5
AW1778763 633 bp mRNA linear EST 18-MAY-2001
LOCUS EST259642 tomato susceptible, Cornell Lycopersicon esculentum cDNA
DEFINITION clone cLES6C20, mRNA sequence.
ACCESSION AW1778763
VERSION AW1778763.1 GI:5276804
KEYWORDS EST.
SOURCE Lycopersicon esculentum
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 633)
AUTHORS D'Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman
,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D.,
Giovannoni,J.J. and Martin,G.B.
TITLE Generation of ESTs from Pseudomonas susceptible tomato
JOURNAL Unpublished (1999)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html

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Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

Lycopersicon.  
1 (bases 1 to 719)

REFERENCE  
AUTHORS  
D'Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E.,  
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman  
.C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D.,  
Giovannoni,J.J. and Martin,G.B.  
Generation of ESTs from *Pseudomonas* susceptible tomato  
Unpublished (1999)  
COMMENT  
Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>  
5 prime sequence.

FEATURES  
source  
1. 719  
/organism="Lycopersicon esculentum"  
/cultivar="RI1-13 (Rio Grande x Money Maker)"  
/db\_xref="taxon:4081"  
/clone="cLES6C20"  
/clone\_lib="tomato susceptible, Cornell"  
/tissue\_type="leaf"  
/dev\_stage="4-week old"  
/lab\_host="SOLR"  
/note="vector: pBluescript SK(-); Site1: EcoRI; Site2:  
XhoI; cLES - Tomato *Pseudomonas* Susceptible EST Library.  
Directionally cloned cDNAs inserted into pBluescript SK(-)  
) at 5' end with EcoRI and 3' end with XhoI site"

BASE COUNT 213 a 93 c 153 g 260 t

ORIGIN

Query Match 31.1%; Score 153; DB 9; Length 719;  
Best Local Similarity 64.7%; Pred. No. 2.2e-35;  
Matches 244; Conservative 0; Mismatches 130; Indels 3; Gaps 1;

Qy 94 tggtaactggcttggtaactgtttgatgacctgctaactgtttagtactagtgtt 153  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 148 TGGTCTACTGGCTTTGTGATGTTCTCTCATATCTCGAGTTGTTGTTAACTTGCTGG 207

Qy 154 tgccttgatcacctttggacagattctgaaataactaacaagaagcaacttcagt 213  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 208 TGTCCATGTATTCATTGGCAAAATGCTGAAATGTGCAAGAACAGTATTTCTGT 267

Qy 214 gggagtagaggtgcattatattgttgc---gggactgacaggattgcctagcctat 270  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 268 GGTCCAAGTGGAGCTTATATTTTATAGAAGCATTAACAGGATGCGGATGATTTAT 327

Qy 271 tcctgctctcacaggtcctaaatgaggggccaatgatctgggaaggcacccttggtt 330  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 328 TCATGTTTTATCTGACAAAAATGAGAAAAACAATACATGTTACCAGAAAGCCCTGTGGG 387

Qy 331 gattgcttgatcatgtattctgtaacctgtgctctcttggcaagaatacacagagctt 390  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 388 GACTGTTTGCTTCATATTTTGTGTGAATGTTGTGCTTTATGCCAAGAACAATCGTGAAC 447

Qy 391 aagaacgtggcttgatagggaatagggtggcaagctaataatgatagacaaagccgg 450  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 448 AAACATCGTGATGATGACATGCTATTGGTTGGCAAGGAATATGGATAACCAAAATGGA 507

Qy 451 ggagttaccatgcccc 467  
||||| ||||| |||||  
Db 508 GGAATAGCAATGGCTCC 524

RESULT 8  
AI778837  
LOCUS  
DEFINITION  
EST259716 tomato susceptible, Cornell Lycopersicon esculentum CDNA  
clone cLES6R8, mRNA sequence.  
ACCESSION  
VERSION  
AI778837  
AI778837.1 GI:5276878

EST.  
SOURCE  
ORGANISM  
tomato.  
Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
1 (bases 1 to 720)  
D' Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E.,  
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman  
C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D.,  
Giovannoni,J.J. and Martin,G.B.  
Generation of ESTs from Pseudomonas susceptible tomato  
Unpublished (1999)  
Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>  
5 prime sequence.

FEATURES  
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1..720  
Location/Qualifiers  
/organism="Lycopersicon esculentum"  
/cultivar="RII-13 (Rio Grande x Money Maker)"  
/db\_xref="taxon:4081"  
/clone="cLES6K8"  
/clone\_lib="tomato susceptible, Cornell"  
/tissue\_type="leaf"  
/dev\_stage="4-week old"  
/lab\_host="SOLR"  
/note="Vector: pBlueScript SK(-); Site\_1: EcoRI; Site\_2:  
xhoI; cLES - Tomato Pseudomonas Susceptible EST Library.  
Directionally cloned cDNAs inserted into pBlueScript SK(-  
) at 5' end with EcoRI and 3' end with XhoI site"  
BASE COUNT 213 a 93 c 153 g 260 t 1 others  
ORIGIN

Query Match 31.1%; Score 153; DB 9; Length 720;  
Best Local Similarity 64.7%; Pred.No. 2.2e-35;  
Matches 244; Conservedity 0; Mismatches 130; Indels 3; Gaps 1;  
QY 94 tggccaatggtcttctgactgcttttgatgacctgctaactgttagttactagtgtt 153  
Db 148 TGGTCTACTGGCGTTTGTGTGATGTGTTCTCTGATATCTCGAGTTGTTTAACTTGCTGG 207  
QY 154 tgccttgatcaccttgagcagattctgaaatactaaacaagaacaactctatgt 213  
Db 208 TGTCCATGTATACATTTTGGACAAATTTGCTGAAATTTGTCGACAAAGGACAGTTCTTGT 267  
QY 214 ggaagttaggtgcatttatattgttgcct---gggaactgacaggttagcctagctatat 270  
Db 268 GGTGCAAGTGGAGCTTTATATTTTTTAAATGAGCATTAACAGGATGTGGATGTATTAT 327  
QY 271 tcctgctctcacaggtctcaaaatgaggggcaaatgatctctggaagaggcaccttgtgtt 330  
Db 328 TCATGTTTTTATCGTACAAAATGAGAAACAATACATGTTACCAGAAAGCCCTTGTGGG 387  
QY 331 gattgtccttgaaatgattctcttgaaaccttgctctcttggcaagaatacagagacctt 390  
Db 388 GACTGTTTGGCTTCATTTTGTGTGAATGTTGTGCTTTATGCCAAGAACAATCGTGAACTC 447  
QY 391 aagaacccgtggcttggatatgggaataagggtggcaagctaatatggataagacaagccgg 450  
Db 448 AAACATCGTGGATGACATGTCCTATTGTTGGTGGCAAGGAATATGGATAACCAAAATGGA 507  
QY 451 ggaagttaaccatgcccc 467  
Db 508 GGAATACATATGGCTCC 524

RESULT 9  
AW040794

LOCUS AW040794 544 bp mRNA linear EST 18-MAY-2001  
 DEFINITION EST283658 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA  
 clone cLET10H19, mRNA sequence.  
 ACCESSION AW040794  
 VERSION AW040794.1 GI:5899548  
 KEYWORDS EST.  
 SOURCE tomato.  
 ORGANISM Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
 Lycopersicon.  
 REFERENCE 1 (bases 1 to 544)  
 AUTHORS D'Ascenzo,M., He,X., Lyman,J., Holt,I.E., Liang,F., Upton,J.,  
 Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W.,  
 Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni  
 J.  
 TITLE Generation of ESTs from tomato leaf tissue  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: CUGI  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 5 prime sequence.  
 FEATURES  
 Location/Qualifiers  
 source 1..544  
 /organism="Lycopersicon esculentum"  
 /cultivar="Rio Grande PtoR"  
 /db\_xref="taxon:4081"  
 /clone="cLET10H19"  
 /clone\_lib="tomato mixed elicitor, BTI"  
 /tissue\_type="leaf"  
 /dev\_stage="4-6 week old plants"  
 /lab\_host="XLL-Blue MRF,"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI; cLET - Inoculated with a variety of disease response  
 elicitors. Plants exposed to 2,6 dichloroisonicotinic  
 acid, BTH, jasmonic acid, ethylene, fenthion, EIX,  
 okadaic acid, or systemin prior to tissue harvest. ECORI  
 site was destroyed during cloning."  
 BASE COUNT 154 a 90 c 117 g 183 t  
 ORIGIN  
 Query Match 30.8%; Score 151.4; DB 9; Length 544;  
 Best Local Similarity 64.5%; Pred. No. 6e-35;  
 Matches 243; Conservative 0; Mismatches 131; Indels 3; Gaps 1;  
 QY 94 tggctcaactggttttgcactgttttgatgacctgtctaactgttttagttagttagt 153  
 DB 148 TGCTCTACTGGGCTTTGCTGATTTCTCTGATATCTCGAGTTGTTGTTAACTTCTGG 207  
 QY 154 tgccttgatcacctttggacagattctgaaataactaaacaaagaaacactcatgt 213  
 DB 208 TGTCATGATTTACATTTGGACAAATGCTGAAATGTCGACAAAGAACAGTTCTTGT 267  
 QY 214 gggagtagaggtgcattattgttggct---gggactgacaggttgcttagcctatat 270  
 DB 268 GGTGCAAGTGGACCTTTATTTTAAATAGAAGCATTAACAGGATGTGGATGATTTAT 327  
 QY 271 tctgtcttacaggtctataaagtgggggcaataatgactctggaagaggcaacctgtgtt 330  
 DB 328 TCATGTTTTTATCGTACAAAAATGAGAAAAACAATACATGTTACCAAGAAAGCCCTTGGG 387  
 QY 331 gattgtctgtacatattctgtgacctgtgtctcttggcaagaataacagagagctt 390  
 DB 388 GACTGTTCCTCATTTTGTGTGAATGTTGTGCTTTATGCCAAGAAATCGTGAACTC 447  
 QY 391 aagaacccgtggtttgatatgggaatagggtggcaagctaaatgtagtagacaaagccgg 450  
 DB 448 AAACATCGTGGATGACATGCTATTGTTGGCAAGGAAATATGATGAACCAAAATGGA 507

QY 451 ggagttaccatgcccc 467  
 DB 508 GGGATAGCAATGGCTCC 524  
 RESULT 10  
 LOCUS AW775220  
 DEFINITION EST256320 tomato resistant, Cornell Lycopersicon esculentum cDNA  
 clone cLER14L22, mRNA sequence.  
 ACCESSION AW775220  
 VERSION AW775220.1 GI:5273261  
 KEYWORDS EST.  
 SOURCE tomato.  
 ORGANISM Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
 Lycopersicon.  
 REFERENCE 1 (bases 1 to 620)  
 AUTHORS D'Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E.,  
 Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman  
 C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D.,  
 Giovannoni,J.J. and Martin,G.B.  
 TITLE Generation of ESTs from Pseudomonas resistant tomato  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: CUGI  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 5 prime sequence.  
 FEATURES  
 Location/Qualifiers  
 source 1..620  
 /organism="Lycopersicon esculentum"  
 /cultivar="Ril-12 (35S::Pto in Rio Grande x Money Maker)"  
 /db\_xref="taxon:4081"  
 /clone="cLER14L22"  
 /clone\_lib="tomato resistant, Cornell"  
 /tissue\_type="leaf"  
 /dev\_stage="4-week old"  
 /lab\_host="SOLR"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI; cLER - Tomato Pseudomonas Resistant EST Library.  
 Directionally cloned cDNAs inserted into pBluescript SK(-  
 ) at 5' end with EcoRI and 3' end with XhoI site."  
 BASE COUNT 184 a 85 c 135 g 215 t  
 ORIGIN  
 Query Match 30.8%; Score 151.4; DB 9; Length 620;  
 Best Local Similarity 64.5%; Pred. No. 6.3e-35;  
 Matches 243; Conservative 0; Mismatches 131; Indels 3; Gaps 1;  
 QY 94 tggctcaactggttttgcactgttttgatgacctgtctaactgttttagttagttagt 153  
 DB 102 TGCTCTACTGGGCTTTGCTGATTTCTCTGATATCTCGAGTTGTTGTTAACTTCTGG 161  
 QY 154 tgccttgatcacctttggacagattctgaaataactaaacaaagaaacactcatgt 213  
 DB 162 TGTCATGATTTACATTTGGACAAATGCTGAAATGTCGACAAAGAACAGTTCTTGT 221  
 QY 214 gggagtagaggtgcattattgttggct---gggactgacaggttgcttagcctatat 270  
 DB 222 GGTGCAAGTGGACCTTTATTTTAAATAGAAGCATTAACAGGATGTGGATGATTTAT 281  
 QY 271 tctgtcttacaggtctataaagtgggggcaataatgactctggaagaggcaacctgtgtt 330  
 DB 282 TCATGTTTTTATCGTACAAAAATGAGAAAAACAATACATGTTACCAAGAAAGCCCTTGGG 341  
 QY 331 gattgtctgtacatattctgtgacctgtgtctcttggcaagaataacagagagctt 390  
 DB 342 GACTGTTCCTCATTTTGTGTGAATGTTGTGCTTTATGCCAAGAAATCGTGAACTC 401





BASE COUNT 146 a 90 c 109 g 180 t  
ORIGIN  
6' ) at 5' end with EcoRI and 3' end with XhoI site."  
Query Match 30.2%; Score 148.4; DB 9; Length 525;  
Best Local Similarity 64.2%; Pred. No. 4.8e-34;  
Matches 240; Conservative 0; Mismatches 131; Indels 3; Gaps 1;  
Qy 94 tggctcaactggtctgttcacactgtttgatgacctgctgaactgttttagttactagtgtt 153  
Db 148 TGGTCTACTGGCTTTGTGATGTCTCTGATATCTCGAGTTGCTGTTAACTTGCCTGG 207  
Qy 154 tgccttctgatacactcttggacagattctctgaaatactaaacaaaggaaacttcgt 213  
Db 208 TGTCCATGATTACATTTGGCAAAATGCTGAAATGTCGACAAAGGAACAGTTCTTGT 267  
Qy 214 gggagtagagtgcaattattttgtct---ggactgacagagattccctagcctatat 270  
Db 268 GTGCAAGTGGAGCTTTATATTTTTTAATAGAAGCATTAACAGGATGTTGGATGTTATT 327  
Qy 271 tctctcttcacagctcaaaatgagggggcaaatatctctggaaggagcaccctgtgtt 330  
Db 328 TCATGTTTTTATCGTACAAAATGAGAAACAATACATGTTACCGAAGGCCCTTGTGGG 387  
Qy 331 gattctctgtacatgtattctgtgaacctgtgtctcttcccaagaatacagagagctt 390  
Db 388 GACTGTTTGCTTCATTTTGTGTGTAATGTTGTCTGTTATGCAAGAACATCGTGAAC 447  
Qy 391 aagaaccctggcttgataggggaatagggggaagtaataatgatagacaaagccgg 450  
Db 448 AAACATCGTGGATATGACATGCTTATGTTGGTGGCAAGAAATATAGTAACCAAAATGGA 507  
Qy 451 ggagttaccatgcc 464  
Db 508 GGGATAGCAATGGC 521

RESULT 15  
BM176887  
LOCUS  
DEFINITION saj74805.yl Gm-cl074 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-cl074-2313 5' similar to TR:Q9SX24 Q9SX24 F24J5.15 PROTEIN. ; , mRNA linear EST 06-DEC-2001  
ACCESSION BM176887  
VERSION BM176887  
KEYWORDS EST.  
SOURCE soybean.  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
REFERENCE 1 (bases 1 to 415)  
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpeliding,J., Coryell,V., Khanna,A., Bolla,B., Marr,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.  
Public Soybean EST Project  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site: www.resgen.com

Trace considered overall poor quality  
Seq primer: -40RP from Gibco  
High quality sequence stop: 1.  
FEATURES  
Location/Qualifiers  
Source  
1..415  
/organism="Glycine max"  
/db\_xref="taxon:3847"  
/clone="SOYBEAN CLONE ID: Gm-cl074-2313"  
/clone\_lib="Gm-cl074"  
/tissue\_type="seedlings induced for HR (hypersensitive response)"  
/dev\_stage="9-11 day old"  
/lab\_host="DH10B"  
/note="vector: pBluescript II SK+; Site\_1: EcoRI; Site\_2: XhoI; The cDNA library was constructed from mRNA isolated from 9-11 day old seedlings that were induced for HR (hypersensitive response) by vacuum infiltrating plant tissue with Pseudomonas syringae pv. glycinea carrying the avrB gene (Genetics 141:1597-1604). Plant tissue (expanded unifoliate leaves) was collected at 2, 4, 8, 12, 24, 36, and 53 hrs after inoculation and their mRNA pooled equally for cDNA construction. The library was prepared using the Stratagene pBluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA insert is protected from XhoI digestion via methylation during first strand synthesis. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. Plant care, inoculations, and library construction were performed by Steve Clough (Lila Vodkin lab, University of Illinois)."  
BASE COUNT 89 a 92 c 114 g 120 t  
ORIGIN  
Query Match 30.0%; Score 147.6; DB 10; Length 415;  
Best Local Similarity 63.8%; Pred. No. 7.7e-34;  
Matches 241; Conservative 0; Mismatches 134; Indels 3; Gaps 1;  
Qy 94 tggctcaactggtctgttcacactgttttgatgacctgctgaactgttttagttactagtgtt 153  
Db 2 TGGTCCACCGCCTCTGTGACTGCTTCTCCGAATCTGGAACATGTTGCATGACGCTTGG 61  
Qy 154 tgccttctgatacactcttggacagattctctgaaatactaaacaaaggaaacttcagt 213  
Db 62 TGTCCATGTTTACTCTTTGGCCGAGTTGCAGAAATTTGTTGACAGGGATCCACATCATGT 121  
Qy 214 gggagtagagtgcaattattttgtct---gggactgacagagattgcctagcctatat 270  
Db 122 GGTGCTAGTGGGGCTCTGTATACCTTTTATTTGCTGAGTCATTTGGCTGTGGCTGCTATAC 181  
Qy 271 tctgtcttcacagctcaaatagggggcaaatatgatctggaagagcgaccttggtt 330  
Db 182 TCTTGCTTCTACCGCCCAAGATGAGACGACAGTATGCTCTAAAGGGAATGTTGTTTCG 241  
Qy 331 gattgtctgtacatgtattctgtgaacctgtgtctcttcccaagaatacagaagctt 390  
Db 242 GATTGCTTGAATCAATGTTGCTTCTGCGAGCCCTGCGCCCTCTGTCAAGAAATATCGTAGCT 301  
Qy 391 aagaaccgtggcttctgatatgggaatagggtggcaagcctaataatgatagacaaagccgg 450  
Db 302 CAACACCGTGGATTTCATGATGATTTATTTGGTGGCGCATGAAATGTCGACACGAAGTCG 361  
Qy 451 ggagttaccatgccctt 468  
Db 362 GGAGTAGCCATGACTGCT 379

Search completed: July 15, 2002, 07:56:22  
Job time: 4795 sec

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 07:56:27 ; Search time 177.53 seconds  
(without alignments)  
4758.192 Million cell updates/sec

Title: US-09-898-659-1  
Perfect score: 492  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues  
Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	123.6	25.1	523	21 AAC45096	Arabidopsis thalia
3	114	23.2	456	21 AAC46412	Arabidopsis thalia
4	105.6	21.5	675	21 AAC37426	Arabidopsis thalia
5	80.2	16.3	673	21 AAC35065	Arabidopsis thalia
6	78.6	16.0	692	19 AAV66762	Pathogen response
7	60.4	12.3	1044	21 AAC45640	Arabidopsis thalia
8	60.4	12.3	1046	21 AAC33819	Arabidopsis thalia
9	53.4	10.9	292	21 AAC32768	Arabidopsis thalia

10	51.4	10.4	749	21 AAC48702	Arabidopsis thalia
11	51.4	10.4	793	21 AAC36679	Arabidopsis thalia
12	47	9.6	958	21 AAC35015	Arabidopsis thalia
13	45.4	9.2	953	21 AAC50407	Arabidopsis thalia
14	40.6	8.3	1897	21 AAC49629	Arabidopsis thalia
15	40.6	8.3	1898	21 AAC36743	Arabidopsis thalia
16	39.6	8.0	1341	18 AAV74759	Staphylococcus aur
17	34.2	7.0	429	21 AAC04289	Human secreted pro
18	34.2	7.0	34980	22 AAH68527	C glutamyl-L-pro
19	33.8	6.9	7607	16 AAQ49754	prK gene LptK-2.
20	33.8	6.9	7607	16 AAQ03097	Protein tyrosine-k
21	33.6	6.8	479	21 AAZ43011	Human 5' EST sola
22	33.6	6.8	602	20 AAV08840	Gene No. 30 encodi
23	33.6	6.8	697	22 AAH68584	Human protein HP10
24	33.6	6.8	703	20 AAZ40821	Secreted protein E
25	33.6	6.8	795	21 AAAG4336	Clone 2790708 of a
26	33.6	6.8	795	21 AAAG4336	cDNA sequence #537
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28	33.6	6.8	891	21 AAC98118	Human colon cancer
29	33.6	6.8	1183	22 AAI86728	Human polynucleoti
30	33.2	6.7	829	21 AAC34836	Arabidopsis thalia
31	33.2	6.7	3222	19 AAX14584	H. pylori GPO 167
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33	32.8	6.7	477	22 ABA26363	Probe #4829 for ge
34	32.8	6.7	477	22 AAI36348	Probe #5034 used t
35	32.8	6.7	6407	24 ABL32943	Human immune syste
36	32.6	6.6	3006	21 AAAG1054	Asparagus asparagi
37	32.2	6.5	761	20 AAZ33842	Tobacco plant resi
38	32	6.5	762	20 AAZ17581	Human gene express
39	32	6.5	3254	22 AAH29739	S cerevisiae apopt
40	32	6.5	6255	24 ABL32960	Human immune syste
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ALIGNMENTS

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KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
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OS Arabidopsis thaliana.  
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PD 06-SEP-2000.  
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PF 25-FEB-2000; 2000EP-0301439.  
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XX metabolic pathway; promoter; termination sequence; ss.  
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PR 29-OCT-1999; 99US-0162142.

Query Match 21.5%; Score 105.6; DB 21; Length 675;

Best Local Similarity 58.5%; Pred. No. 6.8e-26;

Matches 227; Conservative 0; Mismatches 149; Indels 12; Gaps 2;

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Qy 317 aggcacctgtgtgattgtctgtacatgtattctgtgaacctgtgtctcttggccaag 376
Db 630 atgcgccttgtgacattgttgatgttcaactgttgccttgctggtgtgtcttggccaag 689

Qy 377 aatacagagagccttaagaacccgttggcttggatgggaatagggtggccaagctaata 436
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Qy 437 at 438
Db 750 at 751

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XX AAC33819;
XX AAC33819;
XX 17-OCT-2000 (first entry)
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XX Arabidopsis thaliana.
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
XX OS Arabidopsis thaliana.
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PR 29-SEP-1999;	99US-0156596.	PN	EP1033405-A2.
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Qy 317	aggccacctgtgtgtgattgtcttgcattgtgtaacctgtgtctctttgcccaag 376		
Db 632	atgcgccttgtgcatcgttcactgttgcactgtgtgcactgtgtgtcttgtgccagg 691		
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AC AAC32768;			
XX 17-OCT-2000	(first entry)		
DT Arabidopsis thaliana	DNA fragment SEQ ID NO: 580.		
DE Arabidopsis thaliana	genetic mapping; gene expression control;		
XX Hybridisation assay;			

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PR	29-OCT-1999;	9905-0162142.

Query Match 10.9%; Score 53.4; DB 21; Length 292;

Best Local Similarity 59.6%; Pred: No. 4.8e-08;  
Matches 90; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

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[illegible]

Qy 154 Tgccccttgatcacctttggacagatttctgaatactaaacaaagacacttcatt 213

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QY 214 gggagtagagggtgcattatatattgtttgctgg 241

RESULT 10

AAC48702

ID AAC48/U2 standard; DNA; 749 BP.  
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AAC48702;

XX  
DT 18-OCT-20[illegible]

DE ARABIDOPSIS THALIANA DNA FRAGMENT SEQ ID NO: 58448. XX XX

KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

PN EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 04-MAY-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132484.

PR 06-MAY-1999; 99US-0132485.

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PR 07-MAY-1999; 99US-0132487.

PR 11-MAY-1999; 99US-0132863.

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PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

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PR 08-JUN-1999; 99US-0138094.

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PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.

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PR 28-JUN-1999; 99US-0140823.

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PR 01-JUL-1999; 99US-0141842.

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PR 02-JUL-1999; 99US-0142055.

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PR 15-JUL-1999; 99US-0144005.

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PR 19-JUL-1999; 99US-0144335.

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PR 20-JUL-1999; 99US-0144884.

PR 21-JUL-1999; 99US-0144814.

PR 21-JUL-1999; 99US-0145086.

PR 21-JUL-1999; 99US-0145088.

PR 22-JUL-1999; 99US-0145085.

PR 22-JUL-1999; 99US-0145087.

PR 22-JUL-1999; 99US-0145089.

PR 22-JUL-1999; 99US-0145192.

PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145218.

PR 23-JUL-1999; 99US-0145224.

PR 26-JUL-1999; 99US-0145276.

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PR 27-JUL-1999; 99US-0145919.

PR 28-JUL-1999; 99US-0145951.

PR 02-AUG-1999; 99US-0146386.

PR 02-AUG-1999; 99US-0146388.

PR 02-AUG-1999; 99US-0146389.

PR 03-AUG-1999; 99US-0147038.

PR 04-AUG-1999; 99US-0147204.

PR 04-AUG-1999; 99US-0147302.

PR 05-AUG-1999; 99US-0147192.

PR 05-AUG-1999; 99US-0147260.

PR 06-AUG-1999; 99US-0147303.

PR 06-AUG-1999; 99US-0147416.

PR 09-AUG-1999; 99US-0147493.

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PR 10-AUG-1999; 99US-0148171.

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PR 17-AUG-1999; 99US-0149175.

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PR 23-AUG-1999; 99US-0149902.

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PR 25-AUG-1999; 99US-0150566.

PR 26-AUG-1999; 99US-0150884.

PR 27-AUG-1999; 99US-0151065.

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PR 27-AUG-1999; 99US-0151080.

PR 30-AUG-1999; 99US-0151303.

PR 31-AUG-1999; 99US-0151438.

PR	01-SEP-1999;	99US-0151930.	
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PR	13-SEP-1999;	99US-0153758.	
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PR	28-SEP-1999;	99US-0156458.	
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PR	08-OCT-1999;	99US-0158232.	
PR	12-OCT-1999;	99US-0158369.	
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PR	29-OCT-1999;	99US-0162142.	
Query Match 10.4%; Score 51.4; DB 21; Length 749;			
Best Local Similarity 60.3%; Pred. No. 4e-07;			
Matches 85; Conservative 0; Mismatches 56; Indels 0; Gaps 0;			
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Db	416	tatgtctgcgggtaccgcgaatcattaagagccaagtacaaatttacaggagggtccatgt	475
QY	328	gttgattgtcttgaatcatgtattctgtgaaccttgtctcttgcgaagaatacacagag	387
Db	476	ggggattttgtaacacactcttctgcacttgtgtgccatttgcgaagaatacacagag	535
QY	388	cttaagaaccgtggtttgat	408
Db	536	attcagagaacaagcagtggt	556
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XX	AC AAC36679;		
XX	AC AAC36679;		
DT	17-OCT-2000 (first entry)		
XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 14687.		

XX	Hybridisation assay; genetic mapping; gene expression control;
KW	protein identification; signal transduction pathway;
KW	metabolic pathway; promoter; termination sequence; ss.
XX	Arabidopsis thaliana.
OS	EP1033405-A2.
XX	06-SEP-2000.
XX	25-FEB-2000; 2000EP-0301439.
XX	25-FEB-1999; 99US-0121825.
PR	05-MAR-1999; 99US-0123180.
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PR	23-MAR-1999; 99US-0126264.
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PR	08-APR-1999; 99US-0128234.
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PR	16-APR-1999; 99US-0129845.
PR	19-APR-1999; 99US-0130077.
PR	23-APR-1999; 99US-0130449.
PR	23-APR-1999; 99US-0130510.
PR	28-APR-1999; 99US-0130891.
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PR	16-JUL-1999;	99US-0144085.	PR	07-OCT-1999;	99US-0158029.
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PR	26-JUL-1999;	99US-0145276.	PR	25-OCT-1999;	99US-0161404.
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PR	04-AUG-1999;	99US-0147302.	Query Match 10.4%; Score 51.4; DB 21; Length 793;		
PR	05-AUG-1999;	99US-0147192.	Best Local Similarity 60.3%; Pred. No. 4.le-07;		
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PR	13-AUG-1999;	99US-0148565.	Qy		
PR	13-AUG-1999;	99US-0148684.	Db		
PR	16-AUG-1999;	99US-0149388.	Qy		
PR	17-AUG-1999;	99US-0149175.	Db		
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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 8699.  
XX Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX EP1033405-A2.  
PN XX  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0123788.  
PR 23-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
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Qy	359	cttgctctcttgcagaatacacagaagccttaagaaccgtggctttgata	409
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XX	XX	Hybridisation assay; genetic mapping; gene expression control;	
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KW		protein identification; signal transduction pathway;	
XX		metabolic pathway; promoter; termination sequence; ss.	
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Qy 175 cagatttctgaataactaaacaaaggaacaaactctcatgtggagtagaggtgcatatat 234  
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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 14922.  
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KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
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Search completed: July 15, 2002, 09:18:48  
Job time: 4941 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 06:36:37 ; Search time 41.88 seconds  
(without alignments)  
2885.666 Million cell updates/sec

Title: US-09-898-659-1  
Perfect score: 492  
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Scoring table: IDENTITY\_NUC  
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Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	33.8	6.9	7607	5	PCT-US95-04228-19
5	33.6	6.8	703	4	US-09-247-155-79
6	32.6	6.6	7218	1	US-08-232-463-14
7	31.6	6.4	731	4	US-08-998-416-254
8	31.6	6.4	3907	3	US-08-475-742-1
9	31.4	6.4	5261	1	US-08-045-806-3
10	31.4	6.4	5261	1	US-08-366-051B-3
11	30.6	6.2	1607	1	US-08-446-908-1
12	30.6	6.2	1607	1	US-08-231-205A-1
13	30.6	6.2	1607	2	US-08-871-161-1
14	30.6	6.2	7917	2	US-08-167-854-1
15	30.4	6.2	7218	1	US-08-232-463-14
16	29.2	5.9	6840	4	US-08-980-241-8
17	29	5.9	1785	4	US-09-377-155-8
18	29	5.9	1785	4	US-09-669-974-8
19	28.6	5.8	383	1	US-08-620-467A-10
20	28.6	5.8	383	1	US-08-348-572-10
21	28.6	5.8	383	3	US-09-041-090B-10
22	28.4	5.8	1697	1	US-08-472-028A-9
23	28.4	5.8	1697	4	US-09-071-296-9
24	28.4	5.8	1697	4	US-09-196-268-9
25	28.4	5.8	1697	4	US-09-015-683-9
26	28.4	5.8	1697	4	US-09-191-998-9
27	28.2	5.7	552	2	US-08-078-311-18

28	28.2	5.7	552	2	US-08-460-402-18	Sequence 18, Appl
29	28.2	5.7	1216	2	US-08-078-311-20	Sequence 20, Appl
30	28.2	5.7	1216	2	US-08-460-402-20	Sequence 20, Appl
31	28.2	5.7	1307	2	US-08-078-311-17	Sequence 17, Appl
32	28.2	5.7	1307	2	US-08-460-402-17	Sequence 17, Appl
33	28.2	5.7	1623	1	US-08-121-202-3	Sequence 3, Appl
34	28.2	5.7	1644	4	US-08-821-994-71	Sequence 71, Appl
35	28.2	5.7	2046	1	US-08-184-327A-1	Sequence 1, Appl
36	28.2	5.7	2046	5	PCT-US95-00670-1	Sequence 1, Appl
37	28.2	5.7	4334	2	US-08-670-707A-38	Sequence 38, Appl
38	28.2	5.7	4334	4	US-09-037-601-38	Sequence 38, Appl
39	28.2	5.7	6402	2	US-08-670-707A-36	Sequence 36, Appl
40	28.2	5.7	6402	4	US-09-037-601-36	Sequence 36, Appl
41	28	5.7	3846	2	US-08-845-161A-5	Sequence 5, Appl
42	28	5.7	3846	4	US-09-270-751-5	Sequence 5, Appl
43	27.8	5.7	7493	1	US-08-212-133A-7	Sequence 7, Appl
44	27.8	5.7	7493	1	US-08-474-503-5	Sequence 5, Appl
45	27.8	5.7	7493	2	US-08-670-707A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1  
US-08-426-509A-5  
; Sequence 5, Application US/08426509A  
; Patent No. 6326469  
; GENERAL INFORMATION:  
; APPLICANT: Ollrich,, Axel  
; APPLICANT: Gishizsky,, Mikhail  
; APPLICANT: Sures,, Irman G.  
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN  
; TITLE OF INVENTION: TYROSINE KINASES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York,  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/426,509A  
; FILING DATE: 21-APR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/232,545  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi,, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7683-0074-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-9741  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2770 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; US-08-426-509A-5

Query Match 6.9%; Score 33.8; DB 4; Length 2770;  
Best Local Similarity 49.2%; Pred. No. 0.14;  
Matches 89; Conservative 0; Mismatches 92; Indels 0; Gaps 0;









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Db 2441 TACAAATCTGAATGGATTCTATGCCCTTATACACAGAACTTTATTCCTCTAATCAGCCT 2500
QY 66 atctgccccgggaccaccacggcggtggtcaactggctcttggtaactggtttgatga 125
Db 2501 GTATTACCACAAATCCCAATGTACAGAGCTGGACTACCTATGGGGAGTTTGAACCA 2560
QY 126 cctgctaactggttagttactagttgtcccttggatcccttgatcaccttggacagattctga 185
Db 2561 TCCCATACCCCACTACTT-CTAGTTTAGAAGATTTTGTCACCTGTTTACAACCTTCTCTGA 2619
QY 186 aatactaacaagaagaacttca 210
Db 2620 AAACCAAAAGCATGGATTAATCCA 2644

RESULT 10
US-08-366-051B-3
; Sequence 3, Application US/08366051B
; Patent No. 5650283
; GENERAL INFORMATION:
; APPLICANT: Bradfield, Christopher A.
; APPLICANT: Dolwick, Kristin M.
; APPLICANT: Carver, Lucy A.
; TITLE OF INVENTION: An Receptor cDNAs and Genetically
; TITLE OF INVENTION: Engineered Cells for Detecting Agonists to the Ah
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
; STREET: 100 South Wacker Drive, Suite 960
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/366,051B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Tilton, Timothy L.
; REGISTRATION NUMBER: 16,926
; REFERENCE/DOCKET NUMBER: NU-9207-CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)-456-8000
; TELEFAX: (312)-456-7776
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5261 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 383..2927
; US-08-366-051B-3

Query Match 6.4%; Score 31.4; DB 1; Length 5261;
Best Local Similarity 50.2%; Pred. No 1.3;
Matches 103; Conservative 0; Mismatches 101; Indels 1; Gaps 1;

QY 6 tccaacggttaggataatactaggtgataaacaacacacttatgttctcctcactatgt 65
Db 2441 TACAAATCTGAATGGATTCTATGCCCTTATACACAGAACTTTATTCCTCTAATCAGCCT 2500
QY 66 atctgccccgggaccaccacggcggtggtcaactggctcttggtaactggtttgatga 125
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Db 2501 GTATTACCACAAATCCCAATGTACAGAGCTGGACTACCTATGGGGAGTTTGAACCA 2560
QY 126 cctgctaactggttagttactagttgtcccttggatcccttgatcaccttggacagattctga 185
Db 2561 TCCCATACCCCACTACTT-CTAGTTTAGAAGATTTTGTCACCTGTTTACAACCTTCTCTGA 2619
QY 186 aatactaacaagaagaacttca 210
Db 2620 AAACCAAAAGCATGGATTAATCCA 2644

RESULT 11
US-08-446-908-1/c
; Sequence 1, Application US/08446908
; Patent No. 5705149
; GENERAL INFORMATION:
; APPLICANT: Namen, Anthony E.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mochizuki, Diane Y.
; TITLE OF INVENTION: Interleukin-7 and Antibodies Reactive
; TITLE OF INVENTION: Therewith
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,908
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/231,205
; FILING DATE: 21-APR-1994
; APPLICATION NUMBER: US 07/957,649
; FILING DATE: 06-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,438
; FILING DATE: 13-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/255,209
; FILING DATE: 07-OCT-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/113,566
; FILING DATE: 26-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2104-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: mull-7
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: 549..1013
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 549..623
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 624..1010
US-08-446-908-1

Query Match          6.2%; Score 30.6; DB 1; Length 1607;
Best Local Similarity 53.8%; Pred. No. 1.3;
Matches 63; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

Qy 254 gattgcctagcctattcctcgtctctacaggctcaaaatgaggggcaaatatgatctgg 313
Db 845 GAATTCCTCAGTATTCATTTTAAAGAAATGGCTTCAACTTCCGAGCAGCAGGATTAG 786

Qy 314 aagaggcaccttggtgattgcttctgtacatgtattctgtgaaccttgctcttt 370
Db 785 AAAGCAGCTTCTTGTGTATCATCATACATACATGTTTCTAAAAAAGTTTGGTTCATT 729

RESULT 12
US-08-231-205A-1/c
; Sequence 1, Application US/08231205A
; Patent No. 5714585
; GENERAL INFORMATION:
; APPLICANT: Namen, Anthony E.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mochizuki, Diane Y.
; TITLE OF INVENTION: Interleukin-7 and Antibodies Reactive
; TITLE OF INVENTION: Therewith
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231.205A
; FILING DATE: 21-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/957,649
; FILING DATE: 06-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,438
; FILING DATE: 13-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/255,209
; FILING DATE: 07-OCT-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/113,566
; FILING DATE: 26-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2104-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: mUIL-7
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 549..1013
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 549..623
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 624..1010
US-08-231-205A-1

Query Match          6.2%; Score 30.6; DB 1; Length 1607;
Best Local Similarity 53.8%; Pred. No. 1.3;
Matches 63; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

Qy 254 gattgcctagcctattcctcgtctctacaggctcaaaatgaggggcaaatatgatctgg 313
Db 845 GAATTCCTCAGTATTCATTTTAAAGAAATGGCTTCAACTTCCGAGCAGCAGGATTAG 786

Qy 314 aagaggcaccttggtgattgcttctgtacatgtattctgtgaaccttgctcttt 370
Db 785 AAAGCAGCTTCTTGTGTATCATCATACATACATGTTTCTAAAAAAGTTTGGTTCATT 729

RESULT 13
US-08-871-161-1/c
; Sequence 1, Application US/08871161
; Patent No. 5965122
; GENERAL INFORMATION:
; APPLICANT: Namen, Anthony E.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mochizuki, Diane Y.
; TITLE OF INVENTION: Interleukin-7 and Antibodies Reactive
; TITLE OF INVENTION: Therewith
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871.161
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,908
; FILING DATE: 22-MAY-1995
; APPLICATION NUMBER: US 08/231,205
; FILING DATE: 21-APR-1994
; APPLICATION NUMBER: US 07/957,649
; FILING DATE: 06-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,438
; FILING DATE: 13-APR-1990
; PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: US 07/255,209  
/ FILING DATE: 07-OCT-1988  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 07/113,566  
/ FILING DATE: 26-OCT-1987  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Seese, Kathryn A.  
/ REGISTRATION NUMBER: 32,172  
/ REFERENCE/DOCKET NUMBER: 2104-D  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (206) 587-0430  
/ TELEFAX: (206) 233-0644  
/ INFORMATION FOR SEQ ID NO: 1:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 1607 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: cDNA to mRNA  
/ HYPOTHETICAL: NO  
/ ANTI-SENSE: NO  
/ IMMEDIATE SOURCE:  
/ CLONE: null-7  
/ FEATURE:  
/ NAME/KEY: CDS  
/ LOCATION: 549..1013  
/ FEATURE:  
/ NAME/KEY: sig\_peptide  
/ LOCATION: 549..623  
/ FEATURE:  
/ NAME/KEY: mat\_peptide  
/ LOCATION: 624..1010  
/ US-08-871-161-1

Query Match 6.2%; Score 30.6; DB 2; Length 1607;  
Best Local Similarity 53.8%; Pred. No. 1.3;  
Matches 63; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 254 gattgctagctatattctctctacaggctctaaatgagggggcaatgatctgg 313  
DB 845 GAATCTTCACTATATCAATTTAAGAAATTCCTCACTTCGAGCAGCAGATTAG 786  
QY 314 aagaggcaactgtgttgattgtctgtacatgtattctgtgaacctgtgtcttt 370  
DB 785 AAAAGCAGCTTCCTTGTATCATACATACATGTTTCTAAAAAGTTTGGTTCAIT 729

RESULT 14  
US-08-167-854-1/c  
/ Sequence 1, Application US/08167854  
/ Patent No. 5952487  
/ GENERAL INFORMATION:  
/ APPLICANT: Phillip, Wolfgang  
/ APPLICANT: Sapp, Martin  
/ APPLICANT: Cole, Stewart  
/ APPLICANT: Honore, Nadine  
/ TITLE OF INVENTION: DNA Sequences of the Papillomavirus  
/ NUMBER OF SEQUENCES: 2  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
/ STREET: 1300 I Street, N.W.  
/ CITY: Washington  
/ STATE: D.C.  
/ COUNTRY: USA  
/ ZIP: 20005-3315  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ OPERATING SYSTEM: IBM PC compatible  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/167,854  
/ FILING DATE: 10-FEB-1994  
/ CLASSIFICATION: 435  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Potter, Jane E.R.  
/ REGISTRATION NUMBER: 33,332  
/ REFERENCE/DOCKET NUMBER: 02356.0067-00000  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 202-408-4000  
/ TELEFAX: 202-408-4400  
/ INFORMATION FOR SEQ ID NO: 1:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 7917 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: DNA (genomic)  
/ US-08-167-854-1

Query Match 6.2%; Score 30.6; DB 2; Length 7917;  
Best Local Similarity 60.0%; Pred. No. 2.9;  
Matches 51; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 129 tgctaaactgttagttactagtgttgccctgtatccacctttggcacagattctgaaat 188  
DB 1044 TGCTTGTGTTTATTAATAAGGCTTGTGCATGCTACCTGCTTTGTATGTATTACTGTACT 985  
QY 189 actaaacaaagggaacacttcgt 213  
DB 984 ATTATCTACAAAATCCACAGATCT 960

RESULT 15  
US-08-232-463-14  
/ Sequence 14, Application US/08232463  
/ Patent No. 5670367  
/ GENERAL INFORMATION:  
/ APPLICANT: DORNER, F.  
/ APPLICANT: SCHEIFLINGER, F.  
/ APPLICANT: FALKNER, F. G.  
/ TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
/ NUMBER OF SEQUENCES: 52  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Foley & Lardner  
/ STREET: 1800 Diagonal Road, Suite 500  
/ CITY: Alexandria  
/ STATE: VA  
/ COUNTRY: USA  
/ ZIP: 22313-0299  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/232,463  
/ FILING DATE:  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US/07/935,313  
/ FILING DATE:  
/ APPLICATION NUMBER: EP 91 114 300.6  
/ FILING DATE: 26-AUG-1991  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: BENT, Stephen A.  
/ REGISTRATION NUMBER: 29,768  
/ REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (703)836-9300  
/ TELEFAX: (703)683-4109  
/ TELEX: 899149



; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: pTZgpt-F1s  
US-08-232-463-14

Query Match 6.2%; Score 30.4; DB 1; Length 7218;  
Best Local Similarity 6.8%; Pred. NO. 3.2;  
Matches 10; Conservative 85; Mismatches 51; Indels 0; Gaps 0;  
Qy 43 ccttatgttcctcctcactatgtatctgccccgcgaccaccacgcgcggtgtcaact 102  
Db 1306 YY 1365  
Qy 103 ggtctttgtcactgtttttagtaccctgttaactgttttagttactagtgtttgccctgt 162  
Db 1366 YY 1425  
Qy 163 atcaccttggacagatttctgaaat 188  
Db 1426 YYYYYYYYGTACCAAAATCTCTAT 1451

Search completed: July 15, 2002, 08:28:01  
Job time: 6684 sec



Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	403.5	43.8	160	2	E96710		hypothetical protein F7J15.18
2	365.5	39.7	224	2	G96527		unknown protein
3	288	31.3	190	2	A96562		hypothetical protein
4	270.5	29.4	174	2	G96710		hypothetical protein
5	193	21.0	244	2	B84885		hypothetical protein
6	164	17.8	242	2	F84788		hypothetical protein
7	123	13.4	447	2	T04702		hypothetical protein
8	115	12.5	417	2	D84556		hypothetical protein
9	104.5	11.3	230	2	T02853		hypothetical protein
10	98.5	10.7	460	2	F64752		probable melibiose
11	95.5	10.4	782	2	A61625		transacetylase-like protein
12	92.5	10.0	962	2	C5571		subtilisin-like protein
13	91	9.9	969	1	A39490		subtilisin-like protein
14	91	9.9	975	2	C5570		subtilisin-like protein
15	87.5	9.5	1134	1	JN0711		protein-tyrosine kinase
16	84	9.1	232	2	D96663		unknown protein, 5
17	82.5	9.0	136	1	F69857		conserved hypothetical protein-tyrosine kinase
18	82.5	9.0	1136	1	F57845		protein-tyrosine kinase
19	82.5	9.0	3084	1	MM5A		laminin alpha-1 chain
20	81	8.8	300	2	S40837		formate dehydrogenase
21	81	8.8	300	2	C91231		formate dehydrogenase
22	81	8.8	300	2	B86078		formate dehydrogenase
23	81	8.8	300	2	AC0946		formate dehydrogenase
24	81	8.8	1122	2	I54237		protein-tyrosine kinase
25	81	8.8	1123	1	JN0712		protein-tyrosine kinase
26	81	8.8	1135	1	JH0771		protein-tyrosine kinase
27	79.5	8.6	239	2	T16829		hypothetical protein
28	79.5	8.6	3712	2	S18253		laminin alpha-1 chain
29	78	8.5	498	2	D83994		xv-like kinase xvln



A:Gene: At2g45010  
A:Map position: 2

Query Match 21.0%; Score 193; DB 2; Length 244;  
Best Local Similarity 27.7%; Pred. No. 5.7e-11;  
Matches 46; Conservative 23; Mismatches 59; Indels 38; Gaps 4;  
Qy 11 LMKQYPPYVVSAPGTTTARWSTGLCHCFDDPANCCLVTSVCPITFGQISEILNK---G 67  
Db 49 VLPETYEP-----SDENWTTGICCAEDPESCRGLFCPCVLFRGNEAVREIPW 100  
Qy 68 TTSCGSRGAL-----YCLLGLTGLPS-----LYSCFYRSKMRG 100  
Db 101 TOPCVCHAVCVVEGGMALAAVATFSGVIDPOTTVVICGLFFFAWMGCIYSGLFRQELQK 160  
Qy 101 QYDLEAPCVDCLVHVFCPCALCOEYRELKNGRFGDMGIGQANWD 146  
Db 161 KYHLKNAPCDCHMVHCCLLHWCALCOEHRKMKHLSLSDTEASSSTTMD 206

RESULT 6  
F84788  
hypothetical protein At2g37110 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: F84788  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487  
A:Accession: F84788  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-242 <STO>  
A:Cross-references: GB:AE002093; NID:94371290; PIDN:AAD18148.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g37110  
A:Map position: 2

Query Match 17.8%; Score 164; DB 2; Length 242;  
Best Local Similarity 28.8%; Pred. No. 3.2e-08;  
Matches 60; Conservative 17; Mismatches 65; Indels 66; Gaps 9;  
Qy 15 PYVPPHYVSAPCTTT-----ARWSTGL--C-----HCFDDPANCCLVT 49  
Db 41 PLVPPPAAEYGTADGLPVSHGSGVIGPIRRNQNSGLFTCLGRNDEFCSLDLEVCILG 100  
Qy 50 SVCPCITFGQISEILNK--GTTT--CGSRGALY---CLLGLTGLPSLYSCFYRSKMRGQ 101  
Db 101 SVAPCVLGTNAERLGSNPGTFNSHCLTYLGLYFVNSLFGWNC LAPWFSYSSRSATRRK 160  
Qy 102 YDLE-----EAPCVDCLVHVFCPCALCOEYRELKNGRF 135  
Db 161 FNLEGSFEAMNRSCCGCGGCIEDEMQREHLETTTC-DFVTHVLCTCALCOEGRELRRKVL 219  
Qy 136 DMGTGWQANMDRQSGVYTMPYPHAGWTR 163  
Db 220 HPG-----FNAQSTVVVYMPPIEQTMGR 241

RESULT 7  
T04702  
hypothetical protein F4B14.190 - Arabidopsis thaliana  
N:Alternate names: hypothetical protein T19K4.50  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 21-May-1999  
C:Accession: T04702; T05484  
R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hohelsel, J.; Mewes, H.W.; Mayer, K.F.X.  
submitted to the Protein Sequence Database, October 1998

A:Reference number: Z15380  
A:Accession: T04702  
A:Molecule type: DNA  
A:Residues: 1-447 <BEV>  
A:Cross-references: EMBL:AL031986  
A:Experimental source: cultivar Columbia; BAC clone F4B14  
R:Bevan, M.; Wedler, H.; Wambutt, R.; Hohelsel, J.; Mewes, H.W.; Mayer, K.F.X.; Schue  
submitted to the Protein Sequence Database, April 1998  
A:Reference number: Z15418  
A:Accession: T05484  
A:Molecule type: DNA  
A:Residues: 1-447 <BEW>  
A:Cross-references: EMBL:AL022373  
A:Experimental source: cultivar Columbia; BAC clone T19K4  
C:Genetics:  
A:Map position: 4  
A:Introns: 301/2; 340/1; 364/1; 399/3; 431/1  
A:Note: F4B14.190; T19K4.50

Query Match 13.4%; Score 123; DB 2; Length 447;  
Best Local Similarity 30.8%; Pred. No. 0.00045;  
Matches 33; Conservative 13; Mismatches 53; Indels 8; Gaps 2;  
Qy 32 WSTGLCHCFDDPANCCLVTSVCPITFGQISEILN----KGTTCGSRGALYCLLGLTGLP 87  
Db 326 WHTDLLACCSPESLCFKTFPFCGTLAKIATAASNRHISAEACNELMAYSLILSC---- 381  
Qy 88 SLYSCFYRSKMRGQYDLEAPCVDCLVHVFCPCALCOEYRELKNGR 134  
Db 382 CCYTCCVRRRLKRLTNLTGTFIDDFLSHVMCCCALVOELREVEIRG 428

RESULT 8  
D84556  
hypothetical protein At2g17780 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: D84556  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487  
A:Accession: D84556  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-417 <STO>  
A:Cross-references: GB:AE002093; NID:96598810; PIDN:AAB80787.2; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g17780  
A:Map position: 2

Query Match 12.5%; Score 115; DB 2; Length 417;  
Best Local Similarity 29.8%; Pred. No. 0.0024;  
Matches 31; Conservative 12; Mismatches 53; Indels 8; Gaps 2;  
Qy 32 WSTGLCHCFDDPANCCLVTSVCPITFGQISEILN----KGTTCGSRGALYCLLGLTGLP 87  
Db 292 WHADLLDCCSEPCLCRLTFLFPFCGTLAKISTVATSRQISSTEVCKNLIVSYLILSC----- 347  
Qy 88 SLYSCFYRSKMRGQYDLEAPCVDCLVHVFCPCALCOEYRELK 131  
Db 348 CCYTCCIRKKRLKRLTNLTGTCIDDFLSHLMCCCALVOELREVE 391

RESULT 9  
T02853  
hypothetical protein L1439.5 [imported] - Leishmania major (strain Friedlin)  
C:Species: Leishmania major  
C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 19-May-2000

C:Accession: A81463; T02853  
R:Myler, P.J.; Audleman, L.; devos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.;  
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999  
A:Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-c  
A:Reference number: A81455; MUID:99178987  
A:Accession: A81463  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-230 <PYL>  
A:Cross-references: GB:AE001274; NID:g3264850; PIDN:AAC24676.1; PID:g2266921; GSPDB:GN00  
A:Experimental source: strain MHOM/L/81/Friedlin  
C:Genetics:  
A:Gene: L1439.5  
A:Map position: 1

Query Match 11.3%; Score 104.5; DB 2; Length 230;  
Best Local Similarity 25.3%; Pred. No. 0.013;  
Matches 35; Conservative 21; Mismatches 44; Indels 37; Gaps 6;  
QY 32 WSTGLCHCFDDPANCILVTSVCPITFGQISEILNKTTT-----CGSRGALYCL-LGLNG 85  
Db 75 FTSGILNCHESCAVLDACLWCYCTASAHNFMNDTEGLYLPVC---WGLFCVDVGLSA 131  
QY 86 ----LPS---LYSCFYRSKMRGQYDLEEA-----PCVDCILVHVF 117  
Db 132 VSSYLPSSLFHTFYRRAIRRYRLNLSAGAPVNSNTHGSSSGGCDCTTESMLDLITVCF 191  
QY 118 CEPICALCOEYRELKRG 134  
Db 192 CLPCAIAQHQREIMHOG 208

RESULT 10  
F64752  
Probable melibiose carrier protein yagG - Escherichia coli  
N:Alternate names: probable membrane protein yagG  
C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 20-Aug-1999  
C:Accession: F64752  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617  
A:Accession: F64752  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-460 <BLAT>  
A:Cross-references: GB:AE000135; GB:U00096; NID:g1786465; PIDN:AAC73373.1; PID:g1786466;  
A:Experimental source: strain K-12, substrain MG1655  
C:Genetics:  
A:Gene: yagG  
C:Superfamily: melibiose carrier protein  
F:80-96/Domain: transmembrane #status predicted <TM1>  
F:107-123/Domain: transmembrane #status predicted <TM2>  
F:155-171/Domain: transmembrane #status predicted <TM3>  
F:184-200/Domain: transmembrane #status predicted <TM4>  
F:298-314/Domain: transmembrane #status predicted <TM5>  
F:317-333/Domain: transmembrane #status predicted <TM6>  
F:371-387/Domain: transmembrane #status predicted <TM7>  
F:406-422/Domain: transmembrane #status predicted <TM8>

Query Match 10.7%; Score 98.5; DB 2; Length 460;  
Best Local Similarity 29.3%; Pred. No. 0.099;  
Matches 34; Conservative 18; Mismatches 51; Indels 13; Gaps 4;  
QY 1 MYPTGVNIGLMKQPVYPHYVSAPGTTTA----RWSTGLCHCFDDPANCILVTS--VCP 54  
Db 108 YACVTVYILLTVTFVNNVPYCPMGCVITADPKERHALQSRFFLAAGSLAIGTALPL 167  
QY 55 IFFGQISEILNKGTSCSGRGALYCLLLGLTGLPSLYSCFYRSKMRGQYDLEAPCV 110

Db 168 VS-----IIRGDEQGVYFGAM-CVLGLSGVLLVYCFYTKERTFEVQPGSSV 216  
RESULT 11  
A61625  
tenascin-like protein precursor - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C:Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 11-Jan-2000  
C:Accession: A61625; S28463  
R:Baumgartner, S.; Chiquet-Ehrismann, R.  
Mech. Dev. 40, 165-176, 1993  
A:Title: Ten(a), a Drosophila gene related to tenascin, shows selective transcript lo  
A:Reference number: A61625; MUID:93264270  
A:Accession: A61625  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-782 <BAU>  
A:Cross-references: EMBL:X68794  
C:Genetics:  
A:Gene: ten-a  
A:Cross-references: FlyBase:FBgn0004446  
C:Superfamily: unassigned EGF-related proteins; EGF homology  
C:Keywords: tandem repeat  
F:1-62/Domain: signal sequence #status predicted <SIG>  
F:63-782/Product: tenascin-like protein #status predicted <MAT>  
F:497-524/Domain: EGF homology <EGF>

Query Match 10.4%; Score 95.5; DB 2; Length 782;  
Best Local Similarity 22.3%; Pred. No. 0.32;  
Matches 44; Conservative 15; Mismatches 67; Indels 71; Gaps 9;  
QY 17 VPPHYVSAPGTTT-ARWSTGLCHC-----FDDPANCILVTSVCPITFGQISEILNKGT 68  
Db 492 IPVGECEVPNCSSHGRCIEGCHCERGWKGYCDQHDCL-----DPLCSGH 537  
QY 69 TSCGRGALYCLLLGLTGL-----PSLYSCFYRSKMRGQYDLEAPCV----- 110  
Db 538 GTCVA-GQCYCKAGWGEDCGTIDQOYVQCLPGCSEHGTYDLETGOCVCERHWTGPDQSQ 596  
QY 111 -----DCLVHVFCE-----PC-ALCOEYRELKMRGDFMGIGWOANMD 146  
Db 597 AVCSLDCGRNGVCESGKRCNSGWTGNLQDLPCDSRCSEHGCKNGTCVCSQGW----- 651  
QY 147 ROSRGVTMPYPYHAGWTR 163  
Db 652 -NGRHCTLPCCENGCSR 667

RESULT 12  
JC5571  
subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form E-II  
C:Species: Homo sapiens (man)  
C:Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 20-Jun-2000  
C:Accession: JC5571  
R:Mori, K.; Kil, S.; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.;  
J. Biochem. 121, 941-948, 1997  
A:Title: A novel human PACE4 isoform, PACE4E is an active processing protease contain  
A:Reference number: JC5570; MUID:97335942  
A:Accession: JC5571  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-962 <MOR>  
A:Cross-references: DDBJ:D87994; NID:g2330550; PIDN:BA21792.1; PID:g2330551  
A:Experimental source: brain cerebellum  
C:Comment: this enzyme is a processing protease and responsible for processing of var  
ch it is retained intracellularly.  
C:Genetics:  
A:Gene: GDB:PACE4  
A:Cross-references: GDB:131390; OMIM:167405  
A:Map position: 15q26-15q26  
C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology



A:Cross-references: EMBL:X71425; NID:g296610; PIDN:CAA50556.1; PID:g296611  
 R:Sato, T.N.; Qin, Y.; Kozak, C.A.; Audus, K.L.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 9355-9358, 1993  
 A:Title: tie-1 and tie-2 define another class of putative receptor tyrosine kinase genes  
 A:Reference number: S57845; MUID:94022374  
 A:Accession: S57847  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-598, 'L', 600-1134 <SA2>  
 A:Cross-references: EMBL:X71425; NID:g296610; PIDN:CAA50556.1; PID:g296611  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1993  
 R:Korhonen, J.; Partanen, J.; Armstrong, E.; Vaantokari, A.; Elenius, K.; Jalakanen, M.;  
 Blood 80, 2548-2555, 1992  
 A:Title: Enhanced expression of the tie receptor tyrosine kinase in endothelial cells du  
 A:Reference number: A48926; MUID:93043301  
 A:Accession: A48926  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 221-352;740-890 <KOR>  
 A:Note: sequence extracted from NCBI backbone (NCBIP:118660, NCBIP:118662)  
 R:Korhonen, J.; Lahtinen, I.; Halmekeyto, M.; Alhonen, L.; Janne, J.; Dumont, D.; Alitalo  
 Blood 86, 1828-1835, 1995  
 A:Title: Endothelial-specific gene expression directed by the tie gene promoter in vivo.  
 A:Reference number: I52613; MUID:95383653  
 A:Accession: I63403  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-19 <RES>  
 A:Cross-references: GB:S79346; NID:g1086920  
 C:Superfamily: protein-tyrosine kinase, receptor type tie; EGF homology; fibronectin tyf  
 F:Keywords: ARP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosph  
 F:1-21/Domain: signal sequence #status predicted <SIG>  
 F:22-1134/Product: protein-tyrosine kinase, receptor type tie #status predicted <MAT>  
 F:36-105/Domain: immunoglobulin homology <IM1>  
 F:213-253/Domain: EGF homology <EG1>  
 F:257-300/Domain: EGF homology <EG2>  
 F:304-342/Domain: EGF homology <EG3>  
 F:363-426/Domain: immunoglobulin homology <IM2>  
 F:447-528/Domain: fibronectin type III repeat homology <FN3A>  
 F:540-629/Domain: fibronectin type III repeat homology <FN3B>  
 F:638-726/Domain: fibronectin type III repeat homology <FN3C>  
 F:757-782/Domain: transmembrane #status predicted <TM>  
 F:833-1110/Domain: protein kinase homology <KIN>  
 F:841-849/Region: protein kinase ATP-binding motif  
 F:43-103,370-424/Disulfide bonds: #status predicted  
 F:81,159,501,592,705/Binding site: carboxydrate (Asn) (covalent) #status predicted  
 F:866,883,975/Active site: Lys, Glu, Asp #status predicted

Query Match 9.5%; Score 87.5; DB 1; Length 1134;  
 Best Local Similarity 26.2%; Pred. No. 2.7;  
 Matches 34; Conservative 7; Mismatches 48; Indels 41; Gaps 8;  
 QY 26 GTTTARWSTGLCHCFDDPANCLVTSVC-----PCI-----TFGQISEI 63  
 Db 212 GCAGAGRWPG---CVKDCPCGLHGGVCHDHGECVPGFTGTRCQACREGFRGSCQE 268  
 QY 64 LNRGTTSCGSRGALYGLLGLTSLYSCFYRSKMRQYDLEAPC-----VDCLVHVF 117  
 Db 269 QCFGTAGC--RGLTFC-----LPDPYGCSCGSGWRGS-QCQEA-CAPDHFAGDCRLQOQ 318  
 QY 118 CEPCLACQEQ 127  
 Db 319 CQNGGTCDFR 328

Search completed: July 15, 2002, 06:48:13  
 Job time: 95 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 15, 2002, 06:47:53 ; Search time 11.96 Seconds  
(without alignments)  
527.700 Million cell updates/sec

Title: US-09-898-659-2

Perfect score: 921

Sequence: 1 MYPTVGYNLGMLKQYVPPH.....NMDRSGVTWPPYHAGMTR 163

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98.5	10.7	460	1 YAGG_ECOLI	P75683 escherichia
2	91	9.9	969	1 PAC4_HUMAN	P29122 homo sapien
3	87.5	9.5	1134	1 TIE1_MOUSE	Q06806 mus musculus
4	84	9.1	626	1 HCYB_EURCA	Q9nfh9 eurytelma c
5	82.5	9.0	1136	1 TIE1_BOVIN	Q06805 bos taurus
6	82.5	9.0	3084	1 LMA1_MOUSE	P19137 mus musculus
7	81	8.8	300	1 FDOH_ECOLI	P32175 escherichia
8	81	8.8	1122	1 TIE2_MOUSE	Q02858 mus musculus
9	79.5	8.6	3712	1 LMA_DROME	Q00174 drosophila
10	77.5	8.4	798	1 ITB5_MOUSE	Q07309 mus musculus
11	77.5	8.4	1138	1 TIE1_HUMAN	P35590 homo sapien
12	77	8.4	1376	1 CRBH_HUMAN	P82279 homo sapien
13	76	8.3	3075	1 LMA1_HUMAN	P25391 homo sapien
14	75	8.1	1124	1 TIE2_HUMAN	Q02763 homo sapien
15	74.5	8.1	857	1 ENV_HV2RR	Q74126 human immun
16	74.5	8.1	3110	1 LMA2_HUMAN	P24043 homo sapien
17	74	8.0	435	1 TNR3_HUMAN	P36941 homo sapien
18	73.5	8.0	383	1 P013_NASVI	Q03271 nasonia vit
19	73.5	8.0	640	1 UROM_HUMAN	P07911 homo sapien
20	73.5	8.0	937	1 PAC4_RAT	Q63415 rattus norv
21	72.5	7.9	914	1 PERT_MOUSE	P35419 mus musculus
22	72.5	7.9	1104	1 NF1X_HUMAN	Q12986 homo sapien
23	72	7.8	460	1 HYIN_ERWHE	Q47860 erwinia her
24	72	7.8	933	1 PRGR_HUMAN	P06401 homo sapien
25	72	7.8	1801	1 LMB2_RAT	P15800 rattus norv
26	71.5	7.8	755	1 COMP_RAT	P35444 rattus norv
27	71.5	7.8	3106	1 LMA2_MOUSE	Q06675 mus musculus
28	71	7.7	529	1 NRDI_SCHPO	Q09702 schizosacch
29	71	7.7	615	1 FA12_HUMAN	Q00748 homo sapien
30	71	7.7	1592	1 SORL_CHICK	Q98930 g sortilin-
31	70.5	7.7	259	1 PURA_ACTAC	P96771 actinobacil
32	70.5	7.7	1786	1 LMB1_HUMAN	P07942 homo sapien
33	70	7.6	591	1 UL49_EBV	P14347 Epstein-Bar

#### RESULT 1

ID	YAGG_ECOLI	STANDARD;	PRT;	460 AA.
AC	P75683; P71292;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	16-Oct-2001 (Rel. 40, Last annotation update)			
DE	Hypothetical symporter yagG.			
GN	YAGG OR B0270.			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Escherichia.			
OX	NCBI_TaxID=562;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12 / MG1655;			
RX	MEDLINE=97426617; PubMed=9278503;			
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,			
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,			
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,			
RA	Mau B., Shao Y.;			
RT	"The complete genome sequence of Escherichia coli K-12.";			
RL	Science 277:1455-1474(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E.,			
RA	Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,			
RA	Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,			
RA	Davis R.W.;			
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane			
CC	(Potential).			
CC	-!- SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY			
CC	(SGF). STRONG, TO E.COLI Y1CJ.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL; AE000135; AAC73373.1; -			
DR	EMBL; U70214; AAB08691.1; -			
DR	ECODGene; EG13346; yagG.			
DR	InterPro; IPR001927; Na_galact_symp.			
DR	Pfam; PF01236; Na_Galacto_symp; 1			
DR	PROSITE; PS00872; NA_GALACTOSIDE_SYMP; 1.			
KW	Hypothetical protein; Transport; Transmembrane; Inner membrane;			
KW	Symport; Complete proteome.			
FT	TRANSMEM 10 30 POTENTIAL.			
FT	TRANSMEM 31 51 POTENTIAL.			
FT	TRANSMEM 79 99 POTENTIAL.			
FT	TRANSMEM 107 127 POTENTIAL.			
FT	TRANSMEM 151 171 POTENTIAL.			

Q00175 mus musculus  
O63449 rattus norv  
P31696 gallus gall  
P78369 homo sapien  
P13508 caenorhabdi  
Q05793 mus musculus  
P76055 escherichia  
P25266 herpetosiph  
P12336 rattus norv  
P01874 canis famli  
Q07327 drosophila  
Q14202 homo sapien

#### ALIGNMENTS

34 70 7.6 923 1 PRGR\_MOUSE  
35 70 7.6 923 1 PRGR\_RAT  
36 70 7.6 1955 1 AGR1\_CHICK  
37 69.5 7.5 228 1 CLDA\_HUMAN  
38 69 7.5 1295 1 GLPI\_CAEEL  
39 69 7.5 3707 1 PGBM\_MOUSE  
40 68.5 7.4 311 1 YDAO\_ECOLI  
41 68.5 7.4 437 1 MTEI\_HERAU  
42 68.5 7.4 522 1 GTR2\_RAT  
43 68 7.4 450 1 MUC\_CANFA  
44 68 7.4 597 1 ROP\_DROME  
45 68 7.4 1370 1 Z261\_HUMAN

```
FT TRANSMEM 180 200 POTENTIAL.
FT TRANSMEM 263 283 POTENTIAL.
FT TRANSMEM 309 329 POTENTIAL.
FT TRANSMEM 367 387 POTENTIAL.
FT TRANSMEM 406 426 POTENTIAL.
FT CONFLICT 370 370 K -> N (IN REF. 2).
SQ SEQUENCE 460 AA; 50631 MW; AB600588E663C6B7 CRC64;

Query Match 10.7%; Score 98.5; DB 1; Length 460;
Best Local Similarity 29.3%; Pred. No. 0.014;
Matches 34; Conservative 18; Mismatches 51; Indels 13; Gaps 4;

QY 1 MYPTGVNIGLMKQPVYPHYVSAPGTTTA----RWSTGLCHCFDDPANCLVTS--VCP 54
   :| | | | :| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 108 IYACVTYILLTVTFVNVPCMPGVITADPKERHALQSRFFLAAGSLAISGIALPL 167

QY 55 IFPGQISEILNKGTTSCGSRGALYCLLLGLTGLPSLYSCYFRSKMRQYDLEAPCV 110
   :: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 168 VS-----IIGKDEQGVYFGAM-CVLGLSGVLLYVCFEFTTKRYTFEVQPGSSV 216

RESULT 2
PAC4_HUMAN
ID PAC4_HUMAN STANDARD; PRT; 969 AA.
AC P29122; Q15099; Q15100; Q9UEJ1; Q9UEJ2; Q9UEJ7; Q9UEJ8; Q9UEJ9;
AC Q9UEG7; Q9Y4G9; Q9Y4H0; Q9Y4H1;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Paired basic amino acid cleaving enzyme 4 precursor (BC 3.4.21.-)
DE (Subtilisin/kexin-like protease PACE4) (Subtilisin-like proprotein
  convertase 4) (SPC4).
GN PACE4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
[1]
SEQUENCE FROM N.A. (ISOFORMS PACE4A-I AND PACE4B).
RC TISSUE=Hepatoma, and Kidney;
RX MEDLINE=92075167; PubMed=1741956;
RA Kiefer M.C., Tucker J.E., Joh R., Landsberg K.E., Saltman D.,
RA Barr P.J.;
RT "Identification of a second human subtilisin-like protease gene in
  the fes/fps region of chromosome 15.";
RL DNA Cell Biol. 10:757-769(1991).
[2]
SEQUENCE FROM N.A. (ISOFORMS PACE4C AND PACE4D).
RC TISSUE=Placenta;
RX MEDLINE=94235049; PubMed=8179631;
RA Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
RA Matsuda Y.;
RT "Identification of novel cDNAs encoding human kexin-like protease,
  PACE4 isoforms.";
RL Biochem. Biophys. Res. Commun. 200:943-950(1994).
[3]
ERRATUM.
RX MEDLINE=95071480; PubMed=7980617;
RA Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
RA Matsuda Y.;
RT "Identification of novel cDNAs encoding human kexin-like protease,
  PACE4 isoforms.";
RL Biochem. Biophys. Res. Commun. 204:1381-1382(1994).
[4]
SEQUENCE FROM N.A. (ISOFORM PACE4A-II).
RC TISSUE=Placenta;
RX Mori K., Inamaki A., Kii S., Nagamune H., Nagahama M., Tsuji A.,
RA Matsuda Y.;
RT "Identification of a novel PACE4 isoform, PACE4E.";
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
[5]
SEQUENCE FROM N.A. (ISOFORMS PACE4E-I AND PACE4E-II).
```

```
RC TISSUE=Cerebellum;
RX MEDLINE=97335942; PubMed=9192737;
RA Mori K., Kii S., Tsuji A., Nagahama M., Imamaki A., Hayashi K.,
RA Akamatsu T., Nagamune H., Matsuda Y.;
RT "A novel human PACE4 isoform, PACE4E is an active processing protease
  containing a hydrophobic cluster at the carboxy terminus.";
RL J. Biochem. 121:941-948(1997).
[6]
SEQUENCE FROM N.A. (ISOFORMS PACE4A-I; A-II; CS; D; E-I; E-II).
RX MEDLINE=98021085; PubMed=9378725;
RA Tsuji A., Hine C., Tamai Y., Yonemoto K., Mori K., Yoshida S.,
RA Bando M., Sakai E., Mori K., Akamatsu T., Matsuda Y.;
RT "Genomic organization and alternative splicing of human PACE4 (SPC4),
  kexin-like processing endoprotease.";
RL J. Biochem. 122:438-452(1997).
[7]
ALTERNATIVE SPLICING (ISOFORM PACE4CS).
RX MEDLINE=97064242; PubMed=8906861;
RA Zhong M., Benjannet S., Lazure C., Munzer S., Seldah N.G.;
RT "Functional analysis of human PACE4-A and PACE4-C isoforms:
  identification of a new PACE4-CS isoform.";
RL FEBS Lett. 396:31-36(1996).
[8]
CHARACTERIZATION.
RX MEDLINE=99233559; PubMed=10215603;
RA Sucic J.F., Moehring J.M., Inocencio N.M., Luchini J.W.,
RA Moehring T.J.;
RT "Endoprotease PACE4 is Ca2+-dependent and temperature-sensitive and
  can partly rescue the phenotype of a furin-deficient cell strain.";
RL Biochem. J. 339:639-647(1999).
[9]
PROCESSING.
RX MEDLINE=98408849; PubMed=9738469;
RA Nagahama M., Taniguchi T., Hashimoto E., Imamaki A., Mori K.,
RA Tsuji A., Matsuda Y.;
RT "Biosynthetic processing and quaternary interactions of proprotein
  convertase SPC4 (PACE4).";
RL FEBS Lett. 434:155-159(1998).
[1]
FUNCTION: LIKELY TO REPRESENT AN ENDOPEPTIDASE ACTIVITY WITHIN THE
  CONSTITUTIVE SECRETORY PATHWAY, WITH UNIQUE RESTRICTED
  DISTRIBUTION IN BOTH NEUROENDOCRINE AND NON-NEUROENDOCRINE TISSUES
  AND CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF.
[2]
CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
  PROPEPTIDES BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS,
  WHERE XAA CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
[3]
COFACTOR: PACE4A IS PROBABLY CALCIUM-DEPENDENT.
[4]
SUBUNIT: THE PACE4A-I PRECURSOR PROTEIN SEEMS TO EXIST IN THE
  RETICULUM ENDOPLASMIC AS BOTH A MONOMER AND A DIMER-SIZED COMPLEX
  WHEREAS MATURE PACE4A-I EXISTS ONLY AS A MONOMER, SUGGESTING THAT
  PROPEPTIDE CLEAVAGE AFFECTS ITS TERTIARY OR QUATERNARY STRUCTURE.
[5]
SUBCELLULAR LOCATION: PACE4A-I AND PACE4-AII ARE SECRETED. PACE4C
  AND PACE4CS ARE NOT SECRETED AND REMAIN PROBABLY IN ZYMOGEN FORM
  IN ENDOPLASMIC RETICULUM. PACE4E-I AND PACE4E-II ARE RETAINED
  INTRACELLULARLY PROBABLY THROUGH A HYDROPHOBIC CLUSTER IN THEIR C-
  TERMINUS. PACE4B MIGHT BE SECRETED.
[6]
ALTERNATIVE PRODUCTS: 8 ISOFORMS: PACE4A-I/PACE4 (SHOWN HERE),
  PACE4A-II, PACE4B/PACE4.1, PACE4C, PACE4CS, PACE4D, PACE4E-I AND
  PACE4E-II; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORMS PACE4B,
  C, CS AND D MIGHT BE ENZYMATICALLY INACTIVE.
[7]
TISSUE SPECIFICITY: EACH PACE4 ISOFORM EXHIBITS A UNIQUE
  RESTRICTED DISTRIBUTION. PACE4A-I IS EXPRESSED IN HEART, BRAIN,
  PLACENTA, LUNG, SKELETAL MUSCLE, KIDNEY, PANCREAS, BUT AT
  COMPARATIVELY HIGHER LEVELS IN THE LIVER. PACE4A-II IS AT LEAST
  EXPRESSED IN PLACENTA. PACE4B WAS ONLY FOUND IN THE EMBRYONIC
  KIDNEY CELL LINE FROM WHICH IT WAS ISOLATED. PACE4C AND PACE4D ARE
  EXPRESSED IN PLACENTA. PACE4E-I IS EXPRESSED IN CEREBELLUM,
  PLACENTA AND PITUITARY. PACE4E-II IS AT LEAST PRESENT IN
  CEREBELLUM.
[8]
DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
  ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC
  RETICULUM. ISOFORM PACE4D LACKS THE PROPEPTIDE DOMAIN.
[9]
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
  SUBTILASE FAMILY.
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CC -|- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein  
 CC tyrosine phosphate.  
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -|- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING VASCULAR  
 CC ENDOTHELIAL CELLS.  
 CC -|- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC  
 CC DOMAIN.  
 CC -|- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC -|- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -|- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.  
 CC -----  
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 CC -----  
 DR EMBL; X71425; CAA50556.1; -;  
 DR EMBL; X80764; CAA56739.1; -;  
 DR EMBL; X73960; CAA52148.1; -;  
 DR EMBL; S79346; -; NOT\_ANNOTATED\_CDS.  
 DR HSP; P11362; 1FGK.  
 DR MGD; MGI:99906; f1el.  
 DR InterPro; IPR0003561; EGF-like.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003600; Ig\_Like.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00041; fn3; 3.  
 DR Pfam; PF00047; ig; 2.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PRO0109; TYRKINASE.  
 DR SMART; SM00181; EGF; 2.  
 DR SMART; SM00060; FN3; 2.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00410; IG\_Like; 1.  
 DR SMART; SM00219; TyRK; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00022; EGF\_1; 3.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 KW Receptor; Tyrosine-protein kinase; Transferase; Signal; ATP-binding;  
 KW Repeat; EGF-like domain; Transmembrane; Immunoglobulin domain;  
 KW Glycoprotein; Phosphorylation; Multigene family.  
 FT SIGNAL 1 22  
 FT CHAIN 23 1134  
 FT DOMAIN 23 755  
 FT TRANSMEM 756 780  
 FT DOMAIN 781 1134  
 FT DOMAIN 43 103  
 FT DOMAIN 212 254  
 FT DOMAIN 256 301  
 FT DOMAIN 303 343  
 FT DOMAIN 370 424  
 FT DOMAIN 444 538  
 FT DOMAIN 541 635  
 FT DOMAIN 639 740  
 FT DOMAIN 835 1114  
 FT NP\_BIND 841 849  
 FT BINDING 866 866  
 FT ACT\_SITE 975 975  
 FT MOD\_RES 1003 1003  
 FT CARBOHYD 81 81  
 FT CARBOHYD 159 159  
 FT CARBOHYD 501 501  
 FT CARBOHYD 592 592  
 FT CARBOHYD 705 705

FT CONFLICT 599 599 R -> L (IN REF. 1).  
 SQ SEQUENCE 1134 AA; 124698 MW; 0F212ED6C50ACAOE CRC64;  
 Query Match 9.5%; Score 87.5; DB 1; Length 1134;  
 Best Local Similarity 26.2%; Pred. No. 0.47;  
 Matches 34; Conservative 7; Mismatches 48; Indels 41; Gaps 8;  
 QY 26 GTTARWSTGLCHCFDDPANCPLVTSVC-----PCI-----TFGQISEI 63  
 DB 212 GCGAGRWGPG---CVKDCPCCLHGGVCHDHGECVCPGFTGTRCEQACREGFRGSGQOE 268  
 QY 64 LNKGTTCGSGRGALYCLLGLTGLPSLYSCFYRSMRGQYDLLEAPC-----VDCLVHVVF 117  
 DB 269 QCPGTAGC--RGLTFC-----LPDPYGCSCGSGWRGS-QCQEA-CAPDHFADCDRLCQ 318  
 QY 118 CEPCCALCQEQY 127  
 DB 319 CONGGTCDFR 328  
 RESULT 4  
 HCYB\_EURCA STANDARD; PRT; 626 AA.  
 ID HCYB\_EURCA  
 AC Q9NFP9;  
 DT 01-MAR-2002 (Rel. 41, Created)  
 DT 01-MAR-2002 (Rel. 41, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Hemocyanin B chain (Hcb).  
 GN HCB.  
 OS Euryelpma californica (American tarantula).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
 OC Mygalomorphae; Theraphosidae; Aphonopelma.  
 OX NCBI\_TaxID:29932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RX MEDLINE=20564303; PubMed=10961996;  
 RA Voit R., Feldmaier-Fuchs G., Schweikardt T., Decker H., Burmester T.;  
 RT "Complete sequence of the 24-mer hemocyanin of the tarantula Euryelpma  
 RT californicum. Structure and intramolecular evolution of the  
 RT subunits.";  
 RL J. Biol. Chem. 275:39339-39344(2000).  
 CC -|- FUNCTION: HEMOCYANIN ARE COPPER-CONTAINING OXYGEN CARRIERS  
 CC OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND  
 CC ARTHROPODS.  
 CC -|- SUBUNIT: TARANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEVEN  
 CC DIFFERENT CHAINS IDENTIFIED.  
 CC -|- SUBCELLULAR LOCATION: Extracellular.  
 CC -|- MISCELLANEOUS: THE TWO COPPER IONS BOUND EACH HAVE 3 NITROGEN  
 CC LIGANDS (PRESUMABLY CONTRIBUTED BY HIS RESIDUES) AND SHARE A  
 CC BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN  
 CC ADDITION TO BINDING OXYGEN.  
 CC -|- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN  
 CC SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; AJ290429; CAB89498.1; -;  
 DR HSP; P04253; 1LLA.  
 DR InterPro; IPR000896; Hemocyanin.  
 DR InterPro; IPR002227; Tyrosinase.  
 DR PRINTS; PR00187; HAEMOCYANIN.  
 DR PROSITE; PS00209; HEMOCYANIN\_1; 1.  
 DR PROSITE; PS00210; HEMOCYANIN\_2; 1.  
 DR PROSITE; PS00498; TYROSINASE\_2; 1.  
 KW Transport; Oxygen transport; Copper; Glycoprotein; Hemolymph.

```
FT INIT_MET 0 0 BY SIMILARITY.
FT DISULFID 533 581 BY SIMILARITY.
FT METAL 172 172 COPPER 1 (BY SIMILARITY).
FT METAL 176 176 COPPER 1 (BY SIMILARITY).
FT METAL 203 203 COPPER 1 (BY SIMILARITY).
FT METAL 323 323 COPPER 2 (BY SIMILARITY).
FT METAL 327 327 COPPER 2 (BY SIMILARITY).
FT METAL 363 363 COPPER 2 (BY SIMILARITY).
FT METAL 311 311 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 626 AA; 71966 MW; 17E4FB28C91F9974 CRC64;

Query Match 9.1%; Score 84; DB 1; Length 626;
Best Local Similarity 33.8%; Pred. No. 0.57;
Matches 26; Conservative 12; Mismatches 35; Indels 4; Gaps 3;

Qy 81 LGLTGLPSLYCFYSKRGQYDLAEPCVCLVHVFEPCALCQBYRELKNGRFGDMIG 140
Db 38 LGVLGRGLVFCFHEHLKEATQLYEV-LIEC--ESFEFLDCHQAREYVNEGLYVAV 94
Qy 141 WQANDROS-RGVTMP 156
Db 95 SVAILHRQDCRGVSLPP 111

RESULT 5
TIE1_BOVIN STANDARD; PRT; 1136 AA.
AC Q06805;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Tyrosine-protein kinase receptor TIE-1 precursor (EC 2.7.1.112).
GN TIE1 OR TIE-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Endothelial cells;
RX MEDLINE=94022374; PubMed=8415706;
RA Sato T.N., Qin Y., Kozak C.A., Andus K.L.;
RT "Tie-1 and tie-2 define another class of putative receptor tyrosine
RT kinase genes expressed in early embryonic vascular system.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:9355-9358(1993).
CC -1- FUNCTION: PROBABLE PROTEIN TYROSINE-KINASE TRANSMEMBRANE RECEPTOR.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING VASCULAR
CC ENDOTHELIAL CELLS.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; X71423; CAA50554.1; .
DR PIR; S32690; S32690.
DR HSP; P11362; IFCK.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000719; Euk_pkinase.
```

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DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; SM00109; TYRKINASE.
DR PRINTS; SM00181; EGF; 2.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00022; EGF_1; 3.
DR PROSITE; PS00186; EGF_2; 3.
KW Receptor; Tyrosine-protein kinase; Transferase; Signal; ATP-binding;
KW Repeat; EGF-like domain; Transmembrane; Immunoglobulin domain;
KW Glycoprotein; Phosphorylation; Multigene family.
FT SIGNAL 1 23
FT CHAIN 24 1136 TYROSINE-PROTEIN KINASE RECEPTOR TIE-1.
FT DOMAIN 24 757 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 758 782 POTENTIAL.
FT DOMAIN 783 1136 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 43 106 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 212 254 EGF-LIKE 1.
FT DOMAIN 256 301 EGF-LIKE 2.
FT DOMAIN 303 343 EGF-LIKE 3.
FT DOMAIN 370 424 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 444 538 FIBRONECTIN TYPE-III 1.
FT DOMAIN 541 637 FIBRONECTIN TYPE-III 2.
FT DOMAIN 641 742 FIBRONECTIN TYPE-III 3.
FT DOMAIN 837 1116 PROTEIN KINASE.
FT NP_BIND 843 851 ATP (BY SIMILARITY).
FT BINDING 868 868 ATP (BY SIMILARITY).
FT ACT_SITE 977 977 BY SIMILARITY.
FT MOD_RES 1005 1005 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 501 501 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 594 594 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 707 707 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1136 AA; 124953 MW; EFF85804A041BB12 CRC64;

Query Match 9.0%; Score 82.5; DB 1; Length 1136;
Best Local Similarity 26.3%; Pred. No. 1.5;
Matches 35; Conservative 8; Mismatches 43; Indels 47; Gaps 10;

Qy 26 GTTARWST-----GLCHCFDDPANCLVTSVCP-----CI--TFGOI 60
Db 212 GCEARGWQDCTKECPGLHGVCH--DQDGE-----VCPGFTGTRCQACREGRFQGS 265
Qy 61 SEILNKGTTCGSGALYCLLGLTGLPSLYCFYSKRGQYDLAEPC-----VDCUV 114
Db 266 CQECPGTSGC--RGLTFC-----LPDPYGCSCGSGWRGS-QCQEA-CAPGRFGADCHL 315
Qy 115 HVFCPEPCALCQBY 127
Db 316 QCQCQNGGTCDRF 328

RESULT 6
LMAL_MOUSE STANDARD; PRT; 3084 AA.
ID LMAL_MOUSE
AC P19137;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Laminin alpha-1 chain precursor (Laminin A chain).
GN LAMA1 OR LAMA-1 OR LAMA.
```

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE=89034134; PubMed=318280;  
RA Sasaki M., Kleinman H.K., Huber H., Deutzmann R., Yamada Y.;  
RT "Laminin, a multidomain protein. The A chain has a unique globular  
RT domain and homology with the basement membrane proteoglycan and the  
RT laminin B chains.";  
RL J. Biol. Chem. 263:16536-16544(1988).  
RN [2]  
RP SEQUENCE OF 1-339 FROM N.A.  
RX MEDLINE=88225080; PubMed=3267223;  
RA Hartl L., Oberbaumer I., Deutzmann R.;  
RT "The N terminus of laminin A chain is homologous to the B chains.";  
RL Eur. J. Biochem. 173:629-635(1988).  
RN [3]  
RP SEQUENCE OF 2538-3084 FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE=89030693; PubMed=3181157;  
RA Deutzmann R., Huber J., Schmetz K.A., Oberbaumer I., Hartl L.;  
RT "Structural study of long arm fragments of laminin. Evidence for  
RT repetitive C-terminal sequences in the A-chain, not present in the B-  
RT chains.";  
RL Eur. J. Biochem. 177:35-45(1988).  
CC -|- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ  
CC IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF  
CC CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING  
CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.  
CC -|- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE  
CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND  
CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE  
CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.  
CC THE ALPHA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ) AND  
CC LAMININ-3 (S-LAMININ).  
CC -|- SUBCELLULAR LOCATION: Extracellular.  
CC -|- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR  
CC COMPONENT).  
CC -|- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT  
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.  
CC -|- DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.  
CC -|- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).  
CC -|- SIMILARITY: CONTAINS 17 LAMININ EGF-LIKE DOMAINS.  
CC -|- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.  
CC -|- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.  
CC -----  
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CC -----  
CC EMBL: J04064; AAA39410.1; -;  
CC EMBL: X07737; CAA30561.1; -;  
CC EMBL: X13459; CAA31807.1; -;  
CC EMBL: M36775; AAA39406.1; -;  
CC PIR: A31771; WMSA.  
CC HSSP: P02458; 1TLE.  
CC MGD: MGI:99892; Lamal.  
CC InterPro: IPR000561; EGF-like.  
CC InterPro: IPR001886; LamNT.  
CC InterPro: IPR000034; Laminin\_B.  
CC InterPro: IPR002049; Laminin\_EGF.  
CC InterPro: IPR001791; Laminin\_G.  
CC Pfam: PF00052; laminin\_B; 2.  
CC Pfam: PF00053; laminin\_EGF; 15.  
CC Pfam: PF00054; laminin\_G; 5.  
CC Pfam: PF00055; laminin\_Nterm; 1.  
CC PRINTS: PR00011; EGFLAMIN.  
CC ProDom: PD002082; LamNT; 1.  
DR DR ProDom: PD003031; Laminin\_B; 2.  
DR DR SMART: SM00180; EGF\_Lam; 14.  
DR DR SMART: SM00281; LamB; 2.  
DR DR SMART: SM00282; LamG; 5.  
DR DR SMART: SM00136; LamNT; 1.  
DR DR PROSITE: PS00022; EGF\_1; 11.  
DR DR PROSITE: PS01186; EGF\_2; 3.  
DR DR PROSITE: PS01248; LAMININ\_TYPE\_EGF; 15.  
DR DR PROSITE: PS00025; LAM\_G\_DOMAIN; 5.  
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
FT SIGNAL 1 24 POTENTIAL.  
FT CHAIN 25 3084 LAMININ ALPHA-1 CHAIN.  
FT MOD\_RES 25 25 BLOCKED.  
FT DOMAIN 25 276 LAMININ N-TERMINAL (DOMAIN VI).  
FT DOMAIN 277 333 LAMININ EGF-LIKE 1.  
FT DOMAIN 334 403 LAMININ EGF-LIKE 2.  
FT DOMAIN 404 460 LAMININ EGF-LIKE 3.  
FT DOMAIN 461 509 LAMININ EGF-LIKE 4.  
FT DOMAIN 510 519 LAMININ EGF-LIKE 5 (N-TERMINAL).  
FT DOMAIN 520 715 LAMININ DOMAIN IV 1 (DOMAIN IV B).  
FT DOMAIN 716 748 LAMININ EGF-LIKE 5 (C-TERMINAL).  
FT DOMAIN 749 797 LAMININ EGF-LIKE 6.  
FT DOMAIN 798 855 LAMININ EGF-LIKE 7.  
FT DOMAIN 856 908 LAMININ EGF-LIKE 8.  
FT DOMAIN 909 957 LAMININ EGF-LIKE 9.  
FT DOMAIN 958 1004 LAMININ EGF-LIKE 10.  
FT DOMAIN 1005 1050 LAMININ EGF-LIKE 11.  
FT DOMAIN 1051 1096 LAMININ EGF-LIKE 12.  
FT DOMAIN 1097 1156 LAMININ EGF-LIKE 13.  
FT DOMAIN 1157 1368 LAMININ EGF-LIKE 14 (N-TERMINAL).  
FT DOMAIN 1369 1409 LAMININ DOMAIN IV 2 (DOMAIN IV A).  
FT DOMAIN 1410 1458 LAMININ EGF-LIKE 14 (C-TERMINAL).  
FT DOMAIN 1459 1515 LAMININ EGF-LIKE 15.  
FT DOMAIN 1516 1562 LAMININ EGF-LIKE 16.  
FT DOMAIN 1563 2124 LAMININ EGF-LIKE 17.  
FT DOMAIN 1564 2124 DOMAIN II AND I.  
FT DOMAIN 2125 2305 LAMININ G-LIKE 1.  
FT DOMAIN 2313 2489 LAMININ G-LIKE 2.  
FT DOMAIN 2494 2680 LAMININ G-LIKE 3.  
FT DOMAIN 2722 2894 LAMININ G-LIKE 4.  
FT DOMAIN 2899 3079 LAMININ G-LIKE 5.  
FT DOMAIN 1612 1820 COILED COIL (POTENTIAL).  
FT DOMAIN 1869 1903 COILED COIL (POTENTIAL).  
FT DOMAIN 2096 2128 COILED COIL (POTENTIAL).  
FT SITE 1147 1149 CELL ATTACHMENT SITE.  
FT DISULFID 277 286 BY SIMILARITY.  
FT DISULFID 279 297 BY SIMILARITY.  
FT DISULFID 299 308 BY SIMILARITY.  
FT DISULFID 311 331 BY SIMILARITY.  
FT DISULFID 334 343 BY SIMILARITY.  
FT DISULFID 336 368 BY SIMILARITY.  
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FT DISULFID 492 507 BY SIMILARITY.  
FT DISULFID 749 758 BY SIMILARITY.  
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FT DISULFID 767 776 BY SIMILARITY.  
FT DISULFID 779 795 BY SIMILARITY.  
FT DISULFID 798 813 BY SIMILARITY.  
FT DISULFID 800 823 BY SIMILARITY.  
FT DISULFID 826 835 BY SIMILARITY.  
FT DISULFID 838 853 BY SIMILARITY.  
FT DISULFID 856 870 BY SIMILARITY.  
FT DISULFID 858 877 BY SIMILARITY.  
FT DISULFID 880 889 BY SIMILARITY.

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FT DISULFID 892 906 BY SIMILARITY.
FT DISULFID 909 921 BY SIMILARITY.
FT DISULFID 911 928 BY SIMILARITY.
FT DISULFID 930 939 BY SIMILARITY.
FT DISULFID 942 955 BY SIMILARITY.
FT DISULFID 958 970 BY SIMILARITY.
FT DISULFID 960 976 BY SIMILARITY.
FT DISULFID 978 987 BY SIMILARITY.
FT DISULFID 990 1002 BY SIMILARITY.
FT DISULFID 1005 1014 BY SIMILARITY.
FT DISULFID 1007 1021 BY SIMILARITY.
FT DISULFID 1023 1032 BY SIMILARITY.
FT DISULFID 1035 1048 BY SIMILARITY.
FT DISULFID 1051 1063 BY SIMILARITY.
FT DISULFID 1053 1070 BY SIMILARITY.
FT DISULFID 1072 1081 BY SIMILARITY.
FT DISULFID 1084 1094 BY SIMILARITY.
FT DISULFID 1100 1119 BY SIMILARITY.
FT DISULFID 1121 1138 BY SIMILARITY.
FT DISULFID 1142 1158 BY SIMILARITY.
FT DISULFID 1161 1179 BY SIMILARITY.
FT DISULFID 1181 1200 BY SIMILARITY.
FT DISULFID 1211 1230 BY SIMILARITY.
FT DISULFID 1241 1260 BY SIMILARITY.
FT DISULFID 1271 1290 BY SIMILARITY.
FT DISULFID 1301 1320 BY SIMILARITY.
FT DISULFID 1331 1350 BY SIMILARITY.
FT DISULFID 1361 1380 BY SIMILARITY.
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FT DISULFID 1421 1440 BY SIMILARITY.
FT DISULFID 1451 1470 BY SIMILARITY.
FT DISULFID 1481 1500 BY SIMILARITY.
FT DISULFID 1511 1530 BY SIMILARITY.
FT DISULFID 1541 1560 BY SIMILARITY.
FT DISULFID 1563 1586 BY SIMILARITY.
FT DISULFID 1597 1620 BY SIMILARITY.
FT CARBOHYD 45 45 (POTENTIAL).
FT CARBOHYD 79 79 (POTENTIAL).
FT CARBOHYD 370 370 (POTENTIAL).
FT CARBOHYD 374 374 (POTENTIAL).
FT CARBOHYD 531 531 (POTENTIAL).
FT CARBOHYD 562 562 (POTENTIAL).
FT CARBOHYD 672 672 (POTENTIAL).
FT CARBOHYD 770 770 (POTENTIAL).
FT CARBOHYD 857 857 (POTENTIAL).
FT CARBOHYD 914 914 (POTENTIAL).
FT CARBOHYD 959 959 (POTENTIAL).
FT CARBOHYD 969 969 (POTENTIAL).
FT CARBOHYD 1052 1052 (POTENTIAL).
FT CARBOHYD 1344 1344 (POTENTIAL).
FT CARBOHYD 1414 1414 (POTENTIAL).
FT CARBOHYD 1586 1586 (POTENTIAL).
Query Match 9.08; Score 82.5; DB 1; Length 3084;
Best Local Similarity 29.48; Pred. No. 4.2;
Matches 40; Conservative 10; Mismatches 57; Indels 29; Gaps 9;
OY 4 TVGYNLGLMKQYPVPHVPSVAGTTTARWSTGLCHCFDDPANCLVTSVCPCITFGQISEI 63
DB 375 TTGINCEFCIDQYRPHKVSYPDDHPCR-----PCNC---DPVGSLSV-CIKDRHADL 425
OY 64 LN-KGTTSCGRGAL-----YCLGLGLPGLSLYSCFYRSKMGQYDLEAPVCVCLVHV 116
DB 426 ANGKWPQCPCPKRGYAGDKDCRCQGYRGFPNCIPC-----DCRTVGLSLEDPC I----- 475
OY 117 FCEPCALCQEVRELKN 132
DB 476 --EPC-LCKKNVEGKN 488
RESULT 7
ID FDOH_ECOLI STANDARD: PRT; 300 AA.
AC P32175;
DC 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Formate dehydrogenase-O, Iron-sulfur subunit (Formate dehydrogenase-O
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DE beta subunit) (FDH-2 beta subunit) (Aerobic formate dehydrogenase
DE iron-sulfur subunit).
GN FDOH OR B3893.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RC MEDLINE=93347969; PubMed=8346018;
RX Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
RA "Analysis of the Escherichia coli genome. III. DNA sequence of the
RT region from 87.2 to 89.2 minutes.";
RL Nucleic Acids Res. 21:3391-3398(1993).
RN [2]
RN CHARACTERIZATION.
RC STRAIN-K12;
RC MEDLINE=96099298; PubMed=8522521;
RX Aibaou H., Pommier J., Giordano G., Mandrand-Berthelot M.-A.;
RA "Expression and characterization of the Escherichia coli fdo locus
RT and a possible physiological role for aerobic formate
RT dehydrogenase.";
RL J. Bacteriol. 177:7141-7149(1995).
RN [3]
RN TOPOLOGY.
RC MEDLINE=99069333; PubMed=9852007;
RX Benoit S., Aibaou H., Mandrand-Berthelot M.-A.;
RA "Topological analysis of the aerobic membrane-bound formate
RT dehydrogenase of Escherichia coli.";
RL J. Bacteriol. 180:6625-6634(1998).
CC -1- FUNCTION: ALLOWS TO USE FORMATE AS MAJOR ELECTRON DONOR DURING
CC AEROBIC RESPIRATION. THE BETA CHAIN IS AN ELECTRON TRANSFER UNIT
CC CONTAINING 4 CYSTEINE CLUSTERS INVOLVED IN THE FORMATION OF IRON-
CC SULFUR CENTERS. ELECTRONS ARE TRANSFERRED FROM THE GAMMA CHAIN TO
CC THE POLYDENUM COFACTOR OF THE ALPHA SUBUNIT (BY SIMILARITY).
CC -1- SUBUNIT: FORMATE DEHYDROGENASE IS A MEMBRANE-BOUND COMPLEX, FORMED
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
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CC -----
CC EMBL; L19201; AAB03026.1; -.
CC EMBL; AE000484; AAD13455.1; -.
CC PIR; S40837; S40837.
CC HSSP; P00193; 1FDX.
CC EcoGene; EG11857; fdoH.
CC InterPro; IPR001450; 4Fe4S_ferredoxin.
CC Pfam; PF00037; fer4; 1.
CC PRINTS; PR00353; 4FE4SERDOXIN.
CC PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
CC Electron transport; 4Fe-4S; Iron-sulfur; Transmembrane;
CC Complete proteome.
CC DONAIN 1 260 CYTOPLASMIC (PROBABLE).
CC TRANSMEM 261 279 PROBABLE.
CC DONAIN 280 300 PERIPLASMIC (PROBABLE).
CC METAL 39 39 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
CC METAL 42 42 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
CC METAL 45 45 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
CC METAL 49 49 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
CC METAL 100 100 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
CC METAL 103 103 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
CC METAL 108 108 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
CC METAL 112 112 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
CC METAL 133 133 IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY).
CC METAL 136 136 IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY).
CC METAL 139 139 IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY).
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FT DOMAIN 301 341
FT DOMAIN 370 424
FT DOMAIN 444 536
FT DOMAIN 539 633
FT DOMAIN 637 731
FT DOMAIN 822 1094
FT NP_BIND 828 836
FT BINDING 853 853
FT ACT_SITE 962 962
FT CARBOHYD 140 140
FT CARBOHYD 158 158
FT CARBOHYD 399 399
FT CARBOHYD 438 438
FT CARBOHYD 464 464
FT CARBOHYD 558 558
FT CARBOHYD 595 595
FT CARBOHYD 648 648
FT CARBOHYD 690 690
FT MOD_RES 990 990
FT CONFLICT 161 171
FT CONFLICT 538 538
FT CONFLICT 736 736
FT CONFLICT 745 761
FT CONFLICT 786 786
FT CONFLICT 913 913
FT CONFLICT 925 931
FT CONFLICT 1117 1117
SQ SEQUENCE 1122 AA; 125700 MW; F879623D103FFE96 CRC64;

Query Match 8.8%; Score 81; DB 1; Length 1122;
Best Local Similarity 24.1%; Pred. No. 2.1;
Matches 32; Conservative 14; Mismatches 57; Indels 30; Gaps 7;

QY 23 SAPGTTTARWSTGLCHCFDDPANCL-----VTSVCPCTTFGOISILNKGTTSCGS 73
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 221 SPPCTTCK--NGVCH--EDTGECIPPGFMGTCEKACEPTFTGRTKERCSPGEGC-- 274
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
QY 74 RGALYCLGLTGLPSLYSCFYRSKRGVQDLEAPC-----VCLVHVFCPCALQOEYRE 129
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 275 KSYVFC-----LPDPYGCSCATGWRGLQCNEACPSGYGDPCKLRCHCTNEICDRF-- 326
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
QY 130 LKNRGFDMIGWQ 142
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 327 ---QGCLCSQGWQ 336
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :

RESULT 9
LMA_DROME STANDARD; PRT; 3712 AA.
AC Q00174;
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DE 01-MAR-2002 (Rel. 41; Last annotation update)
DE Laminin alpha chain precursor.
GN LANA OR LAMA.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta.
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93049203; PubMed=1425586;
RA Kusche-Gullberg M., Garrison K., Mackrell A.J., Fessler J.H.;
RA Fessler J.H.;
RT "Laminin A chain: expression during Drosophila development and
genomic sequence."
RL EMBO J. 11:4519-4527(1992).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
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RX MEDLINE=94038678; PubMed=8223265;
RA Hencliffe C., Garcia-Alonso L., Tang J., Goodman C.S.;
RT "Genetic analysis of laminin A reveals diverse functions during
morphogenesis in Drosophila."
RL Development 118:325-337(1993).
RN [3]
RX SEQUENCE OF 1762-3712 FROM N.A.
RX MEDLINE=92078147; PubMed=1744083;
RA Garrison K., Mackrell A.J., Fessler J.H.;
RT "Drosophila laminin A chain sequence, interspecies comparison, and
domain structure of a major carboxyl portion."
RL J. Biol. Chem. 266:22899-22904(1991).
CC -!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT, BY INTERACTING
WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CC -!- FUNCTION: DIVERSE FUNCTION MUTATIONS DURING MORPHOGENESIS IN DROSOPHILA.
CC COMPLETE LOSS-OF-FUNCTION MUTATIONS LEAD TO LATE EMBRYONIC
LETHALITY. CERTAIN PARTIAL LOSS-OF-FUNCTION MUTATIONS GIVE RAISE
TO ESCAPER ADULTS, WHICH HAVE ROUGH EYES ASSOCIATED WITH CHANGES
IN CELL FATE AND PATTERN, MISSHAPEN LEGS AND DEFECTS IN WING
STRUCTURE.
CC -!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
MEMBRANES (MAJOR COMPONENT).
CC -!- TISSUE SPECIFICITY: NEWLY FORMED MESODERM AND LATER PROMINENTLY
EXPRESSED IN HEMOCYTES, WHICH ALSO SYNTHESIZE COLLAGEN IV.
CC -!- DEVELOPMENTAL STAGE: DURING MORPHOGENESIS, MOSTLY IN EMBRYO
DEVELOPMENT AT 10-12 HOURS.
CC -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -!- DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.
CC -!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -!- SIMILARITY: CONTAINS 21.5 LAMININ EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV (DOMAIN IV) IS NOT
SIMILAR TO LAMININ DOMAIN IV).
CC -!- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
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DR	PROSITE; PS01186; EGF_2; 5.	1	22	POTENTIAL.
DR	PROSITE; PS01248; LAMININ_TYPE_EGF; 19.	23	3712	LAMININ ALPHA CHAIN.
DR	PROSITE; PS50025; LAM_G_DOMAIN; 5.	25	272	LAMININ N-TERMINAL (DOMAIN VI).
KW	Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;	273	332	LAMININ EGF-LIKE 1.
KW	Laminin EGF-like domain; Cell adhesion; Repeat; Signal.	333	402	LAMININ EGF-LIKE 2.
FT	SIGNAL	403	447	LAMININ EGF-LIKE 3.
FT	CHAIN	448	494	LAMININ EGF-LIKE 4.
FT	DOMAIN	495	540	LAMININ EGF-LIKE 5.
FT	DOMAIN	541	586	LAMININ EGF-LIKE 6.
FT	DOMAIN	587	631	LAMININ EGF-LIKE 7.
FT	DOMAIN	632	676	LAMININ EGF-LIKE 8.
FT	DOMAIN	677	731	LAMININ EGF-LIKE 9.
FT	DOMAIN	732	784	LAMININ EGF-LIKE 10.
FT	DOMAIN	785	815	LAMININ EGF-LIKE 11 (INCOMPLETE).
FT	DOMAIN	816	1374	DOMAIN IV'.
FT	DOMAIN	1375	1420	LAMININ EGF-LIKE 12.
FT	DOMAIN	1421	1465	LAMININ EGF-LIKE 13.
FT	DOMAIN	1466	1513	LAMININ EGF-LIKE 14.
FT	DOMAIN	1514	1564	LAMININ EGF-LIKE 15.
FT	DOMAIN	1565	1574	LAMININ EGF-LIKE 16 (N-TERMINAL).
FT	DOMAIN	1575	1775	LAMININ DOMAIN IV (DOMAIN IV).
FT	DOMAIN	1776	1808	LAMININ EGF-LIKE 16 (C-TERMINAL).
FT	DOMAIN	1809	1858	LAMININ EGF-LIKE 17.
FT	DOMAIN	1859	1916	LAMININ EGF-LIKE 18.
FT	DOMAIN	1917	1969	LAMININ EGF-LIKE 19.
FT	DOMAIN	1970	2016	LAMININ EGF-LIKE 20.
FT	DOMAIN	2017	2063	LAMININ EGF-LIKE 21.
FT	DOMAIN	2064	2111	LAMININ EGF-LIKE 22.
FT	DOMAIN	2112	2671	DOMAIN II AND I.
FT	DOMAIN	2672	2868	LAMININ G-LIKE 1.
FT	DOMAIN	2876	3048	LAMININ G-LIKE 2.
FT	DOMAIN	3055	3223	LAMININ G-LIKE 3.
FT	DOMAIN	3349	3528	LAMININ G-LIKE 4.
FT	DOMAIN	3534	3709	LAMININ G-LIKE 5.
FT	DOMAIN	2178	2249	COILED COIL (POTENTIAL).
FT	DOMAIN	2301	2321	COILED COIL (POTENTIAL).
FT	DOMAIN	2376	2450	COILED COIL (POTENTIAL).
FT	DOMAIN	2541	2676	COILED COIL (POTENTIAL).
FT	DOMAIN	3270	3296	POLY-THR.
FT	DISULFID	273	282	BY SIMILARITY.
FT	DISULFID	275	296	BY SIMILARITY.
FT	DISULFID	298	307	BY SIMILARITY.
FT	DISULFID	310	330	BY SIMILARITY.
FT	DISULFID	333	342	BY SIMILARITY.
FT	DISULFID	335	367	BY SIMILARITY.
FT	DISULFID	370	379	BY SIMILARITY.
FT	DISULFID	382	400	BY SIMILARITY.
FT	DISULFID	403	414	BY SIMILARITY.
FT	DISULFID	405	421	BY SIMILARITY.
FT	DISULFID	423	432	BY SIMILARITY.
FT	DISULFID	435	445	BY SIMILARITY.
FT	DISULFID	448	460	BY SIMILARITY.
FT	DISULFID	450	468	BY SIMILARITY.
FT	DISULFID	470	479	BY SIMILARITY.
FT	DISULFID	482	492	BY SIMILARITY.
FT	DISULFID	495	507	BY SIMILARITY.
FT	DISULFID	497	514	BY SIMILARITY.
FT	DISULFID	516	525	BY SIMILARITY.
FT	DISULFID	528	538	BY SIMILARITY.
FT	DISULFID	541	553	BY SIMILARITY.
FT	DISULFID	543	560	BY SIMILARITY.
FT	DISULFID	562	571	BY SIMILARITY.
FT	DISULFID	574	584	BY SIMILARITY.
FT	DISULFID	587	599	BY SIMILARITY.
FT	DISULFID	589	605	BY SIMILARITY.
FT	DISULFID	607	616	BY SIMILARITY.
FT	DISULFID	619	629	BY SIMILARITY.
FT	DISULFID	632	644	BY SIMILARITY.





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CC EMBL; AF154671; AAF01361.1; --  
CC HSSP; P08709; 1BF9.  
CC MIM; 604210; --  
DR MIM; 600105; --  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001438; EGF\_11.  
DR InterPro; IPR002049; Laminin\_EGF.  
DR InterPro; IPR001791; Laminin\_G.  
DR Pfam; PF00008; EGF; 16.  
DR Pfam; PF00054; Laminin\_G; 3.  
DR PRINTS; PR00010; EGFBL00D.  
DR PRINTS; PR00011; EGF\_LAMININ.  
DR SMART; SM00179; EGF\_CA; 8.  
DR SMART; SM00001; EGF\_like; 8.  
DR SMART; SM00282; LamG; 3.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 10.  
DR PROSITE; PS00022; EGF\_1; 15.  
DR PROSITE; PS01186; EGF\_2; 11.  
DR PROSITE; PS01187; EGF\_CA; 7.  
DR PROSITE; PS00025; LAM\_G\_DOMAIN; 3.  
KW EGF-like domain; Glycoprotein; Repeat; Signal; Disease mutation;  
KW Retinitis pigmentosa; Vision.  
FT SIGNAL 1 25 POTENTIAL.  
FT CHAIN 26 1376 CRUMBS PROTEIN HOMOLOG 1.  
FT DOMAIN 70 108 EGF-LIKE 1.  
FT DOMAIN 110 146 EGF-LIKE 2.  
FT DOMAIN 148 184 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 186 222 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 224 260 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 304 337 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 339 395 EGF-LIKE 7.  
FT DOMAIN 441 481 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 485 670 LAMININ G-LIKE 1.  
FT DOMAIN 672 708 EGF-LIKE 9.  
FT DOMAIN 714 885 LAMININ G-LIKE 2.  
FT DOMAIN 887 923 EGF-LIKE 10.  
FT DOMAIN 950 1137 LAMININ G-LIKE 3.  
FT DOMAIN 1139 1175 EGF-LIKE 11.  
FT DOMAIN 1177 1212 EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 1214 1250 EGF-LIKE 13.  
FT DOMAIN 1255 1295 EGF-LIKE 14.  
FT DOMAIN 1297 1333 EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).  
FT DISULFID 74 85 POTENTIAL.  
FT DISULFID 79 96 POTENTIAL.  
FT DISULFID 98 107 POTENTIAL.  
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FT DISULFID 119 134 POTENTIAL.  
FT DISULFID 136 145 POTENTIAL.  
FT DISULFID 152 163 POTENTIAL.  
FT DISULFID 157 172 POTENTIAL.  
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FT DISULFID 190 201 POTENTIAL.  
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FT DISULFID 233 248 POTENTIAL.  
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FT DISULFID 348 383 POTENTIAL.  
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FT DISULFID 445 456 POTENTIAL.  
FT DISULFID 460 469 POTENTIAL.  
FT DISULFID 471 480 POTENTIAL.  
FT DISULFID 676 687 POTENTIAL.  
FT DISULFID 681 696 POTENTIAL.  
FT DISULFID 698 707 POTENTIAL.  
FT DISULFID 891 902 POTENTIAL.  
FT DISULFID 896 911 POTENTIAL.  
FT DISULFID 913 922 POTENTIAL.  
FT DISULFID 1143 1154 POTENTIAL.  
FT DISULFID 1148 1163 POTENTIAL.  
FT DISULFID 1165 1174 POTENTIAL.  
FT DISULFID 1181 1191 POTENTIAL.  
FT DISULFID 1186 1200 POTENTIAL.  
FT DISULFID 1202 1211 POTENTIAL.  
FT DISULFID 1218 1229 POTENTIAL.  
FT DISULFID 1223 1238 POTENTIAL.  
FT DISULFID 1240 1249 POTENTIAL.  
FT DISULFID 1259 1274 POTENTIAL.  
FT DISULFID 1268 1283 POTENTIAL.  
FT DISULFID 1285 1294 POTENTIAL.  
FT DISULFID 1301 1312 POTENTIAL.  
FT DISULFID 1306 1321 POTENTIAL.  
FT DISULFID 1323 1332 POTENTIAL.  
FT CARBOHYD 30 30 N-LINKED (GLCNAC... (POTENTIAL).  
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FT CARBOHYD 42 42 N-LINKED (GLCNAC... (POTENTIAL).  
FT CARBOHYD 215 215 N-LINKED (GLCNAC... (POTENTIAL).  
FT CARBOHYD 287 287 N-LINKED (GLCNAC... (POTENTIAL).  
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FT CARBOHYD 322 322 N-LINKED (GLCNAC... (POTENTIAL).  
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FT CARBOHYD 453 453 N-LINKED (GLCNAC... (POTENTIAL).  
FT CARBOHYD 550 550 N-LINKED (GLCNAC... (POTENTIAL).  
FT CARBOHYD 561 561 N-LINKED (GLCNAC... (POTENTIAL).  
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FT CARBOHYD 880 880 N-LINKED (GLCNAC... (POTENTIAL).  
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FT CARBOHYD 975 975 N-LINKED (GLCNAC... (POTENTIAL).  
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FT CARBOHYD 1265 1265 N-LINKED (GLCNAC... (POTENTIAL).  
FT CARBOHYD 1273 1273 N-LINKED (GLCNAC... (POTENTIAL).  
FT VARIANT 161 161 A -> V (IN RP12).  
FT VARIANT 250 250 C -> W (IN RP12).  
FT VARIANT 745 745 /FTid=VAR\_011642.  
FT VARIANT 764 764 /FTid=VAR\_011643.  
FT VARIANT 948 948 /FTid=VAR\_011644.  
FT VARIANT 1041 1041 /FTid=VAR\_011645.  
FT VARIANT 1071 1071 /FTid=VAR\_011646.  
FT VARIANT 1100 1100 /FTid=VAR\_011647.  
FT VARIANT 1181 1181 /FTid=VAR\_011648.  
FT VASCULOPATHY.  
FT /FTid=VAR\_011649.  
SQ SEQUENCE 1376 AA; 151412 MW; F380DF2AA046A2FE CRC64;  
Query Match 8.4%; Score 77; DB 1; Length 1376;  
Best local Similarity 23.7%; Pred. No. 6.5;  
Matches 36; Conservative 19; Mismatches 45; Indels 52; Gaps 10;  
QY 18 PPHY-----VSAPGTTTARWSTGLCHCFDDPANCILVTSVCPCITFGQISELNGKTT 69  
DB 99 PPGYSGTICETTTIGSCGRNQCQG-GICH--QDP--IYPVCICPAGYAGRFEIDHDECA 153



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FT DISULFID 399 427 BY SIMILARITY.
FT DISULFID 429 438 BY SIMILARITY.
FT DISULFID 441 451 BY SIMILARITY.
FT DISULFID 454 467 BY SIMILARITY.
FT DISULFID 456 471 BY SIMILARITY.
FT DISULFID 473 482 BY SIMILARITY.
FT DISULFID 485 500 BY SIMILARITY.
FT DISULFID 742 751 BY SIMILARITY.
FT DISULFID 744 757 BY SIMILARITY.
FT DISULFID 760 769 BY SIMILARITY.
FT DISULFID 772 788 BY SIMILARITY.
FT DISULFID 791 806 BY SIMILARITY.
FT DISULFID 793 816 BY SIMILARITY.
FT DISULFID 819 828 BY SIMILARITY.
FT DISULFID 831 846 BY SIMILARITY.
FT DISULFID 849 863 BY SIMILARITY.
FT DISULFID 851 870 BY SIMILARITY.
FT DISULFID 873 882 BY SIMILARITY.
FT DISULFID 885 899 BY SIMILARITY.
FT DISULFID 902 914 BY SIMILARITY.
FT DISULFID 904 921 BY SIMILARITY.
FT DISULFID 923 932 BY SIMILARITY.
FT DISULFID 935 948 BY SIMILARITY.
FT DISULFID 951 963 BY SIMILARITY.
FT DISULFID 953 969 BY SIMILARITY.
FT DISULFID 971 980 BY SIMILARITY.
FT DISULFID 983 995 BY SIMILARITY.
FT DISULFID 998 1007 BY SIMILARITY.
FT DISULFID 1000 1014 BY SIMILARITY.
FT DISULFID 1016 1025 BY SIMILARITY.
FT DISULFID 1028 1041 BY SIMILARITY.
FT DISULFID 1044 1056 BY SIMILARITY.
FT DISULFID 1046 1063 BY SIMILARITY.
FT DISULFID 1065 1074 BY SIMILARITY.
FT DISULFID 1077 1087 BY SIMILARITY.
FT DISULFID 1403 1412 BY SIMILARITY.
FT DISULFID 1405 1419 BY SIMILARITY.
FT DISULFID 1422 1431 BY SIMILARITY.
FT DISULFID 1434 1449 BY SIMILARITY.
FT DISULFID 1452 1466 BY SIMILARITY.
FT DISULFID 1454 1476 BY SIMILARITY.
FT DISULFID 1479 1488 BY SIMILARITY.
FT DISULFID 1491 1506 BY SIMILARITY.
FT DISULFID 1509 1521 BY SIMILARITY.
FT DISULFID 1511 1528 BY SIMILARITY.
FT DISULFID 1530 1539 BY SIMILARITY.
FT DISULFID 1542 1553 BY SIMILARITY.
FT DISULFID 1556 1566 INTERCHAIN (PROBABLE).
FT DISULFID 1560 1560 INTERCHAIN (PROBABLE).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 555 555 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 665 665 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 763 763 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 926 926 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 952 952 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1045 1045 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1407 1407 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1579 1579 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1596 1596 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1678 1678 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1689 1689 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1698 1698 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1717 1717 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1804 1804 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1894 1894 N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 8.3%; Score 76; DB 1; Length 3075;
Best Local Similarity 20.1%; Pred. No. 19;
Matches 32; Conservative 16; Mismatches 55; Indels 56; Gaps 9;
QY 21 YVSAPGTTTARWSTGLCHC-----FDDPANCLVTSVCPICITFGQISE 62
DB 905 HVKGSHSVCHLETGLCDCKPNVWGQCDQLHGYGLDSHGHC---RPCNCVSAGVSVD 961
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QY 63 ILNKGTTSCGRGALYCLLGLTGLPSLYSCFYRKMGRQYDLEAPCVC-LVHV--PCE 119
DB 962 -----CCTDEGQCHCVPVAG-KRCRCAH-----GFYAYQDSCTPCDCHPTQNTCD 1008
QY 120 P-----CALCOEYRELKNGRFGDMGIGWOA 143
DB 1009 PETGECVCPHTQGGKCECED-----GHWGYDAEVGCOA 1043

RESULT 14
TIE2_HUMAN
ID TIE2_HUMAN STANDARD; PRT; 1124 AA.
AC Q02763;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiopoietin 1 receptor precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor TIE-2) (Tyrosine-protein kinase receptor TEK) (P140
DE TEK) (Tunica interna endothelial cell kinase).
GN TEK OR TIE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93173509; PubMed=8382358;
RA Ziegler S.F., Bird T.A., Schneringer J.A., Schooley K.A., Baum P.R.;
RT "Molecular cloning and characterization of a novel receptor protein
RT tyrosine kinase from human placenta.";
RL Oncogene 8:663-670(1993).
RN [2]
RP VARIANT VMC1 TRP-849.
RX MEDLINE=97134665; PubMed=8980225;
RA Vikkula M., Boon L.M., Carraway K.L. III, Calvert J.T., Diamonti A.J.,
RA Goumnerov B., Pasyk K.A., Marchuk D.A., Warman M.L., Cantley L.C.,
RA Mulliken J.B., Olse B.R.;
RT "Vascular dysmorphogenesis caused by an activating mutation in the
RT receptor tyrosine kinase TIE2.";
RL Cell 87:1181-1190(1996).
RN [3]
RP VARIANTS VMC1 TRP-849 AND SER-897.
RX MEDLINE=99299243; PubMed=10369874;
RA Calvert J.T., Riney T.J., Kontos C.D., Cha E.H., Prieto V.G.,
RA Shea C.R., Berg J.N., Nevin N.C., Simpson S.A., Pasyk K.A.,
RA Speer M.C., Peters K.G., Marchuk D.A.;
RT "Allelic and locus heterogeneity in inherited venous malformations.";
RL Hum. Mol. Genet. 8:1279-1289(1999).
CC -!- FUNCTION: THIS PROTEIN IS A PROTEIN TYROSINE-KINASE TRANSMEMBRANE
CC RECEPTOR FOR ANGIOPOIETIN 1. IT MAY CONSTITUTE THE EARLIEST
CC MAMMALIAN ENDOTHelial CELL LINEAGE MARKER. PROBABLY REGULATES
CC ENDOTHelial CELL PROLIFERATION, DIFFERENTIATION AND GUIDES THE
CC PROPER PATTERNING OF ENDOTHelial CELLS DURING BLOOD VESSEL
CC FORMATION.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN ENDOTHelial CELLS
CC AND THEIR PROGENITORS, THE ANGIOBLASTS. HAS BEEN DIRECTLY FOUND
CC IN PLACENTA AND LUNG, WITH A LOWER LEVEL IN UMBILICAL VEIN
CC ENDOTHelial CELLS, BRAIN AND KIDNEY.
CC -!- DISEASE: DEFECTS IN TEK ARE A CAUSE OF DOMINANTLY INHERITED VENOUS
CC MALFORMATIONS (VMC1), AN ERROR OF VASCULAR MORPHOGENESIS
CC CHARACTERIZED BY DILATED, SERPINOUS CHANNELS.
CC -!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN.
CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
```





Search completed: July 15, 2002, 06:51:28  
Job time: 215 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2002, 06:46:57 ; Search time 27.59 Seconds  
(without alignments)  
1022.043 Million cell updates/sec

Title: us-09-898-659-2  
Perfect score: 921  
Sequence: 1 MYPTVGYNLGLMKQPYVPPH.....NMDRSGVTMPYPYHAGMTR 163

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	921	100.0	163	10 Q9LKV6	Q9LKV6 lycopersico
2	899	97.6	163	10 Q9LKV7	Q9LKV7 lycopersico
3	433	47.0	152	10 Q9LQ04	Q9LQ04 arabidopsis
4	403.5	43.8	160	10 Q9SX24	Q9SX24 arabidopsis
5	403	43.8	151	10 Q9LQ02	Q9LQ02 arabidopsis
6	378	41.0	145	10 Q9ZTM8	Q9ZTM8 petunia hyb
7	365.5	39.7	224	10 Q9M9A5	Q9M9A5 arabidopsis
8	358.5	38.9	184	10 Q9LS44	Q9LS44 arabidopsis
9	347	37.7	133	10 Q9LS43	Q9LS43 arabidopsis
10	319.5	34.7	184	10 Q9LS45	Q9LS45 arabidopsis
11	299.5	32.5	161	10 Q94L14	Q94L14 oryza sativ
12	288	31.3	190	10 Q9M815	Q9M815 arabidopsis
13	270.5	29.4	174	10 Q9SX26	Q9SX26 arabidopsis
14	193	21.0	147	10 Q9SDC9	Q9SDC9 oryza sativ
15	193	21.0	238	10 Q9FEE1	Q9FEE1 arabidopsis
16	193	21.0	244	10 Q9SHD7	Q9SHD7 arabidopsis

17	166	18.0	240	10 Q9FGN2	Q9fgn2 arabidopsis
18	166	18.0	241	10 P94032	P94032 arabidopsis
19	164	17.8	242	10 Q9ZQC8	Q9zqc8 arabidopsis
20	156.5	17.0	235	10 Q9FV00	Q9fyq0 oryza sativ
21	153	16.6	525	10 Q94D92	Q94d92 oryza sativ
22	151	16.4	241	10 Q9M5D4	Q9m5d4 chlamydomon
23	135	14.7	112	11 Q9J148	Q9j148 mus musculu
24	134	14.5	115	4 Q9NZF1	Q9nzi1 homo sapien
25	132	14.3	115	4 Q96EJ4	Q96ej4 homo sapien
26	123.5	13.4	440	10 Q9ASR5	Q9asr5 arabidopsis
27	123	13.4	447	10 Q65629	Q65629 arabidopsis
28	119	12.9	111	11 Q9D7R1	Q9d7r1 mus musculu
29	118	12.8	179	4 Q9BYD5	Q9byd5 homo sapien
30	115	12.5	417	10 Q22563	Q22563 arabidopsis
31	108	11.7	253	10 Q943N4	Q943n4 oryza sativ
32	104.5	11.3	230	5 Q15846	Q15846 leishmania
33	95.5	10.4	777	5 Q24550	Q24550 drosophila
34	95.5	10.4	777	5 Q9V1P1	Q9vyp1 drosophila
35	94.5	10.3	641	5 Q9V7I1	Q9v7i1 drosophila
36	93.5	10.2	297	10 Q9FN61	Q9fn61 arabidopsis
37	92	10.0	790	5 Q9GSF3	Q9gsf3 podocoryne
38	91.5	9.9	177	11 Q9DAB1	Q9dab1 mus musculu
39	86.5	9.4	81	10 Q9M5D5	Q9m5d5 chlamydomon
40	85.5	9.3	229	11 Q9QZ1	Q9qz1 mus musculu
41	85.5	9.3	266	11 Q9R1K1	Q9rik1 rattus norv
42	85.5	9.3	337	11 Q9R1K0	Q9rik0 rattus norv
43	85.5	9.3	2764	11 Q9WTS5	Q9wts5 mus musculu
44	85.5	9.3	2765	11 Q9R1K2	Q9rik2 rattus norv
45	84	9.1	232	10 Q9CAJ7	Q9caj7 arabidopsis

ALIGNMENTS

RESULT 1

Q9LKV6	PRELIMINARY;	PRT;	163 AA.
ID	Q9LKV6		
AC	Q9LKV6;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last annotation update)		
DE	ORFX.		
OS	Lycopersicon pennellii (Tomato).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
OC	Asteridae; euasterids I; Solanales; Solanaceae; Solanum.		
OX	NCBI_TaxID=28526;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Frary A., Nesbitt T., Clint, Frary A., Grandillo S., van der Knaap E.,		
RA	Cong B., Liu J., Meller J., Elber R., Alpert K.B., Tanksley S.D.;		
RT	"fw2.2: a quantitative trait locus key to the evolution of tomato		
RT	fruit size".		
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF261775; AAF74287.1; -.		
SQ	SEQUENCE 163 AA; 18062 MW; 0628795F184B4869 CRC64;		

Query Match	100.0%;	Score 921;	DB 10;	Length 163;
Best Local Similarity	100.0%;	Pred. NO. 1.3e-98;		
Matches 163;	Conservative	0; Mismatches	0; Indels	0; Gaps
0;				
Qy	1	MYPTVGYNLGLMKQPYVPPHYVSAPGTTTARWSTGLCHCFDDPANCLVTSVCPCTITFQI	60	
Db	1	MYPTVGYNLGLMKQPYVPPHYVSAPGTTTARWSTGLCHCFDDPANCLVTSVCPCTITFQI	60	
Qy	61	SEILNKGTTCGSGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEAPCVCLVHVHVFCEP	120	
Db	61	SEILNKGTTCGSGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEAPCVCLVHVHVFCEP	120	
Qy	121	CALCQEYRELNRGFDGIGIGHQANMDRQSRGVTMPYPYHAGMTR	163	
Db	121	CALCQEYRELNRGFDGIGIGHQANMDRQSRGVTMPYPYHAGMTR	163	

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RESULT 2
Q9LKV7 PRELIMINARY; PRT; 163 AA.
AC Q9LKV7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ORFX.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asterales; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RA Frary A., Nesbitt T., Clint, Frary A., Grandillo S., van der Knaap E.,
RA Cong B., Liu J., Meller J., Elber R., Alpert K.B., Tanksley S.D.;
RT "fw2.2: a quantitative trait locus key to the evolution of tomato
RT fruit size.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF261774; AAF74286.1; -
SQ SEQUENCE 163 AA; 18061 MW; AA46EA140B7A8803 CRC64;

Query Match 97.6%; Score 899; DB 10; Length 163;
Best Local Similarity 98.2%; Pred. No. 4.6e-96;
Matches 160; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MYPTGVNGLMKQPYVPPHYVAPGTTTARWSTGLCHCFDDPANCPLVTSVCPCTIFGQI 60
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 MYPTGVNPGMPKQPYVPPHYVAPGTTTARWSTGLCHCFDDPANCPLVTSVCPCTIFGQI 60

QY 61 SEILNKGTTCGSGRGALYCLGLTGLTSLYSCFYRSMRGQYDLEAPCVDCLVHVFCPE 120
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 61 SEILNKGTTCGSGRGALYCLGLTGLTSLYSCFYRSMRGQYDLEAPCVDCLVHVFCPE 120

QY 121 CALCQYRELKNGFDMGIGQWQANDRQSRGVTPPYHAGMTR 163
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 121 CALCQYRELKNGFDMGIGQWQANDRQSRGVTPPYHAGMTR 163

RESULT 3
Q91QU4 PRELIMINARY; PRT; 152 AA.
AC Q91QU4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE F10B6.27.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Chao Q., Shinn P., Dunn P., Buehler E., Kahn S., Kim C., Walker M.,
RA Williams S., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A.,
RA Hansen N.F., Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S.,
RA Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G.,
RA Davis R.W., Federspiel N.A., Theologis A., Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome
RT I.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;

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RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chlou J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC006917; AAF79235.1; -
DR InterPro: IPR000152; ASX_hydroxyl.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN.1.
SQ SEQUENCE 152 AA; 16742 MW; BC0655E747D315D1 CRC64;

Query Match 47.0%; Score 433; DB 10; Length 152;
Best Local Similarity 51.0%; Pred. No. 3.3e-42;
Matches 78; Conservative 23; Mismatches 40; Indels 12; Gaps 4;

QY 16 YVPPHYVVSAPGTTTARWSTGLCHCFDDPANCPLVTSVCPCTIFGQISEILNKGTTCGSGRG 75
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 7 HAKPH-----AEGWSTGFCDFSDCNCCITFCWPCITFGVAEIVDRGSTCGTAG 59

QY 76 ALYCLLG-LTGLPSLYSCFYRSMRGQYDLEAPCVDCLVHVFCPEALCQYRELKNGR 134
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 60 ALYALLAVTGCACIYSCFYRSMRGQYNIKGDCTDCLKHFCECLSLTQQYRELKNGR 119

QY 135 FDMGIGQWQANDRQSR--GVTPM--PPYHAGMTR 163
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 120 YDMSLGWAGNVERQNOGGVAMGAPVFOGGMTR 152

RESULT 4
Q9SX24 PRELIMINARY; PRT; 160 AA.
AC Q9SX24;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE F24J5.15 PROTEIN.
GN F24J5.15.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
RA Lee J.M., Li J., Gonzalez A., Liu A., Liu K., Vaysberg M., Sakano H.,
RA Chin C., Choi E., Chlou J., Altafi H., Araujo R., Brooks S.,
RA Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
RA Howing B., Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P.,
RA Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
RT "The sequence of BAC F24J5 from Arabidopsis thaliana chromosome 1.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC008075; RAD4981.1; -
SQ SEQUENCE 160 AA; 17971 MW; 132987DB38E71522 CRC64;

Query Match 43.8%; Score 403.5; DB 10; Length 160;
Best Local Similarity 48.5%; Pred. No. 9e-39;
Matches 80; Conservative 27; Mismatches 41; Indels 17; Gaps 6;

QY 8 NLGLMKQPYVPPHYVAPGTTTAR--WSTGLCHCFDDPANCPLVTSVCPCTIFGQISEILNK 66
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 2 NLSSNDQP-----SQGRIRAKDWSTDLCECWMDSCLTWCPCVAFGRVWDR 53

QY 67 GTTSCGSRGALYCLL-GLTGL--PSLYSCFYRSMRGQYDLEAPCVDCLVHVFCPEAL 123
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RESULT	6	
Q9ZTM8		
ID	Q9ZTM8	PRELIMINARY;
AC	Q9ZTM8;	PRT; 145 AA.

Query Match 39.7%; Score 365.5; DB 10; Length 224;  
Best Local Similarity 41.8%; Pred. No. 3.2e-34;  
Matches 76; Conservative 29; Mismatches 48; Indels 29; Gaps  
Ov 1 MYPTGVNGLMKOP-YVP-----PHYVSPG-----TTTARWSTGLCHC 39









GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2002, 06:46:37 ; Search time 30.38 Seconds  
(without alignments)  
595.952 Million cell updates/sec

Title: US-09-898-659-2

Perfect score: 921

Sequence: 1 MYPTVGYNLGLMKQPVPPH.....NMDRSGVTMPYPYHAGMTR 163

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_032802.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	433	47.0	152	21	Arabidopsis thalia
2	425	46.1	152	21	Arabidopsis thalia
3	403.5	43.8	160	21	Arabidopsis thalia
4	403.5	43.8	173	21	Arabidopsis thalia
5	403	43.8	151	21	Arabidopsis thalia
6	363	39.4	133	21	Arabidopsis thalia
7	289	31.4	190	21	Arabidopsis thalia
8	289	31.4	194	21	Arabidopsis thalia
9	288	31.3	188	19	Pathogen response
10	280.5	30.5	190	21	Arabidopsis thalia
11	280.5	30.5	190	21	Arabidopsis thalia

12	231.5	25.1	90	21	AAG40343	Arabidopsis thalia
13	226	24.5	79	21	AAG40344	Arabidopsis thalia
14	211	22.9	133	21	AAG14720	Arabidopsis thalia
15	211	22.9	133	21	AAG46458	Arabidopsis thalia
16	207	22.3	76	21	AAG04523	Arabidopsis thalia
17	194	21.1	70	21	AAG36901	Arabidopsis thalia
18	193	21.0	198	21	AAG07319	Arabidopsis thalia
19	193	21.0	198	21	AAG38298	Arabidopsis thalia
20	193	21.0	244	21	AAG07318	Arabidopsis thalia
21	193	21.0	244	21	AAG38297	Arabidopsis thalia
22	170	18.5	106	21	AAG10516	Arabidopsis thalia
23	166	18.0	240	21	AAG51030	Arabidopsis thalia
24	166	18.0	241	21	AAG51029	Arabidopsis thalia
25	164	17.8	240	21	AAG10396	Arabidopsis thalia
26	164	17.8	241	21	AAG10395	Arabidopsis thalia
27	164	17.8	242	21	AAG24599	Arabidopsis thalia
28	164	17.8	242	21	AAG30353	Arabidopsis thalia
29	164	17.8	242	21	AAG49966	Arabidopsis thalia
30	140	15.2	169	21	AAG51031	Arabidopsis thalia
31	138	15.0	169	21	AAG10397	Arabidopsis thalia
32	134	14.5	115	21	AA08524	Protein encoded by
33	134	14.5	115	21	AA065397	Human 5' EST relat
34	134	14.5	115	22	AAG93299	Human protein HP10
35	134	14.5	120	21	AA053361	Human colon cancer
36	132	14.3	115	20	AA059693	Secreted protein 4
37	128	13.9	130	21	AAG07320	Arabidopsis thalia
38	128	13.9	130	21	AAG38299	Arabidopsis thalia
39	123	13.4	357	21	AAG14892	Arabidopsis thalia
40	123	13.4	357	21	AAG48943	Arabidopsis thalia
41	123	13.4	384	21	AAG14891	Arabidopsis thalia
42	123	13.4	384	21	AAG48942	Arabidopsis thalia
43	123	13.4	421	21	AAG14890	Arabidopsis thalia
44	123	13.4	421	21	AAG48941	Arabidopsis thalia
45	117.5	12.8	188	21	AAG55093	Arabidopsis thalia

#### ALIGNMENTS

RESULT 1

AAG36900  
ID AAG36900 standard; Protein; 152 AA.

XX AC AAG36900;

XX AC  
DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 45286.

XX KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX OS Arabidopsis thaliana.

XX FN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126284.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

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PR 16-APR-1999; 99US-0129845.

PR 21-APR-1999; 99US-0130077.

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PR 23-APR-1999; 99US-0130510.  
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PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
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Query Match          47.0%; Score 433; DB 21; Length 152;
Best Local Similarity 51.0%; Pred. NO. 3.6e-38;
Matches 78; Conservative 23; Mismatches 40; Indels 12; Gaps

QY 16 YVPPHYVSFGTTTARWSTGLCHCFDDPANCLVTSVPCITFGQISEILNKGTTSCGSRG 75
DB 7 hahph-----aegewstgfcdfcdkcnccitfwcpctifggvaeivdrgstscgtag 59
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QY 76 ALXCLLG-LTGFLPSLXCFSYRSKMRGOYLDEEAPCDLVHVFCEPACALCOEYRELKNRG 134
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QY 135 FDGIGHQANDRQSR--GVTM--PPYHAGMTR 163
DB : || : || : || : || : || : || : || : || : || : || : || : || : ||
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RESULT 2
AAG39510
ID AAG39510 standard; Protein; 152 AA.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
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QY 79 CLL-GLTGLPSLYSCFYRSKMRGOYDLEAPCVDLVHVFCPCALCOEYRELKNRGFD 137  
Db 63 vllaaigtgcylsciyrgkraqynirgdctdclkhfccelcaltqeyrelkhrqfdm 122  
QY 138 GICQANMDRQSR--GVTM--PPYHAGMTR 163  
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KW hybridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.  
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XX PD 06-SEP-2000.  
XX PF 25-FEB-2000; 2000EP-0301439.  
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QY	124	CQEYRELK-NRGFDMGTGWQANDROSR----GVTMPYPYHAGMTR 163	
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XX	KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
XX	KW	termination sequence.	
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PR	22-OCT-1999;	99US-0160980.	PR	06-MAY-1999;	99US-0132487.
PR	22-OCT-1999;	99US-0160981.	PR	07-MAY-1999;	99US-0132863.
PR	22-OCT-1999;	99US-0160989.	PR	11-MAY-1999;	99US-0134256.
PR	22-OCT-1999;	99US-0161404.	PR	14-MAY-1999;	99US-0134218.
PR	25-OCT-1999;	99US-0161405.	PR	14-MAY-1999;	99US-0134219.
PR	25-OCT-1999;	99US-0161406.	PR	14-MAY-1999;	99US-0134221.
PR	26-OCT-1999;	99US-0161359.	PR	14-MAY-1999;	99US-0134370.
PR	26-OCT-1999;	99US-0161360.	PR	18-MAY-1999;	99US-0134768.
PR	26-OCT-1999;	99US-0161361.	PR	19-MAY-1999;	99US-0134941.
PR	28-OCT-1999;	99US-0161920.	PR	20-MAY-1999;	99US-0135124.
PR	28-OCT-1999;	99US-0161992.	PR	21-MAY-1999;	99US-0135353.
PR	28-OCT-1999;	99US-0161993.	PR	24-MAY-1999;	99US-0135629.
PR	29-OCT-1999;	99US-0162142.	PR	25-MAY-1999;	99US-0136021.
Query Match 43.8%; Score 403; DB 21; Length 151;					
Best Local Similarity 48.4%; Pred. No. 5.5e-35;					
Matches 75; Conservative 21; Mismatches 47; Indels 12; Gaps 4;					
Qy	14 QYVPPHTVSAPGTTTARWSTGLCHCFDDPANCLVTSVCPCTITFGQISEILNKGTTSCGS	73	PR	01-JUN-1999;	99US-0137222.
Db	4 qlhaxph-----aqgewstgfcdfadcrnccltccpctitfgqvaeivdrqskcca	56	PR	03-JUN-1999;	99US-0137528.
Qy	74 RGALYCLLGL-TGLPSLYSCYRSRMRCQYDLEAPCVDCLVHVFCPCALCQEVRELKN	132	PR	04-JUN-1999;	99US-0137502.
Db	57 agalymldlitsegrmacyfsgkmraqynikgdgctcdclkhfcncalcaltqgyreikh	116	PR	07-JUN-1999;	99US-0137724.
Qy	133 RCFDNGIGCQANMDROSR--GVTM--PPYHAGMTR	163	PR	08-JUN-1999;	99US-0138094.
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XX			PR	18-JUN-1999;	99US-0139456.
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XX			PR	18-JUN-1999;	99US-0139461.
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XX			PR	01-JUL-1999;	99US-0142154.
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XX			PR	12-JUL-1999;	99US-0143542.
XX	25-FEB-1999; 99US-0121825.		PR	13-JUL-1999;	99US-0143624.
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PR	09-MAR-1999; 99US-0123548.		PR	15-JUL-1999;	99US-0144085.
PR	23-MAR-1999; 99US-0125788.		PR	16-JUL-1999;	99US-0144086.
PR	25-MAR-1999; 99US-0126264.		PR	19-JUL-1999;	99US-0144325.
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PR 04-AUG-1999; 99US-0147204.  
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PR 05-AUG-1999; 99US-0147192.  
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PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
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PR 27-AUG-1999; 99US-0151065.  
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PR 27-AUG-1999; 99US-0151080.  
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PR 01-SEP-1999; 99US-0151930.  
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PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
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PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
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PR 13-OCT-1999; 99US-0159293.

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PR 28-OCT-1999; 99US-0161920.  
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Query Match 39.4%; Score 363; DB 21; Length 133;  
Best Local Similarity 52.3%; Pred. No. 8.5e-31;  
Matches 68; Conservative 24; Mismatches 30; Indels 8; Gaps 4;  
  
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Db 2 dlnsccltcwpcvafgrtaevvdrgstcgvsgamymifmltgygsslsycfyrtkl 61  
  
QY 99 RGQYDLEAPCVDCLVHVFCPCALCOEYRELK-NRGFDWGMIGWQANMDRQSR---GVT 153  
Db 62 raqynlkerpcdccevhfcpcalcqeyrqlqhnrdldlvigwhgnmerharlaastps 121  
  
QY 154 MPYHAGWTR 163  
Db 122 applqapmsr 131  
  
RESULT 7  
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XX  
DT 17-OCT-2000 (first entry)  
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 8870.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
PF 25-FEB-2000; 2000EP-0301439.  
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PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
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PR 28-MAY-1999; 99US-0136782.  
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PR 04-JUN-1999; 99US-0137502.  
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PR 22-JUN-1999; 99US-0139899.  
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PR	21-OCT-1999;	99US-0160814.	PR	05-MAY-1999;	99US-0132485.
PR	21-OCT-1999;	99US-0160815.	PR	06-MAY-1999;	99US-0132486.
PR	22-OCT-1999;	99US-0160980.	PR	06-MAY-1999;	99US-0132487.
PR	22-OCT-1999;	99US-0160981.	PR	07-MAY-1999;	99US-0132863.
PR	22-OCT-1999;	99US-0160989.	PR	11-MAY-1999;	99US-0134256.
PR	23-OCT-1999;	99US-0161404.	PR	14-MAY-1999;	99US-0134218.
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PR	29-OCT-1999;	99US-0162142.	PR	25-MAY-1999;	99US-0136021.
Query Match 31.4%; Score 289; DB 21; Length 190;					99US-0136392.
Best Local Similarity 38.1%; Pred. No. 9.7e-23;					99US-0136782.
Matches 61; Conservative 29; Mismatches 54; Indels 16; Gaps 4;					99US-0137222.
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Db	35	fapnpyqanvnisvgrpwtgltfdcaqadanavlttiivpcvtfggiaevmdegemtclpl 94	PR	04-JUN-1999;	99US-0137502.
QY	74	RGALYCLLGLTGLPSLYSCF-----YRSKMRGQVDLEAPCVDCLVHVFCPCALCQEYR 128	PR	07-JUN-1999;	99US-0137724.
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QY	129	ELKNRGFDGMIGW----QANMDRQSRGVTMPVYHAGMTR 163	PR	10-JUN-1999;	99US-0138540.
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DT	17-OCT-2000 (first entry)				
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 8869.				
XX	XX				
KW	Protein identification; signal transduction pathway; metabolic pathway;				
KW	hybridisation assay; genetic mapping; gene expression control; promoter;				
KW	termination sequence.				
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OS	Arabidopsis thaliana.				
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PD	06-SEP-2000.				
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AC AAG46457;  
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KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
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OS Arabidopsis thaliana.  
XX  
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PD 06-SEP-2000.  
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RESULT 13  
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DT 18-OCT-2000 (first entry)  
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 50046.  
XX KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.  
XX OS Arabidopsis thaliana.  
XX EP1033405-A2.  
XX PD 06-SEP-2000.  
XX PF 25-FEB-2000; 2000EP-0301439.  
XX PR 25-FEB-1999; 99US-0121825.  
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